

97975

From: Chan, Christina  
Sent: Wednesday, July 02, 2003 1:30 PM  
To: Mertz, Prema; STIC-Biotech/ChemLib  
Subject: RE: 09/521,195

**Please rush. Thanks Chris**

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

-----Original Message-----

From: **Mertz, Prema**  
Sent: Wednesday, July 02, 2003 1:02 PM  
To: Chan, Christina  
Subject: 09/521,195

Please conduct an interference search on SEQ ID NO:1-2.

Thanks  
--Prema Mertz--  
Prema Mertz, Ph.D.  
Primary Examiner  
Art Unit 1646  
Mailbox 10D-19  
Crystal Mall 1, Room 10E-01  
United States Patent & Trademark Office  
# (703) 308-4229

Christina-

Please RUSH this search on an after-final for me.

Thanks.

--Prema--

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpn** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapn** and **.rapn**

*The Pending database search results should not be left in the case because they contain data that is confidential.*





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2003, 12:30:34 ; Search time 149 Seconds  
(without alignments)  
2384.214 Million cell updates/sec

Title: US-09-521-195B-1

Perfect score: 2845  
Sequence: 1 MRDYDEVIAFLGEMGFQRL.....KTRDSMETENPKVLTAF 551

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*  
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3: /cgn2\_6/ptodata/1/paa/US07.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US080.COMB.pep.\*  
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25: /cgn2\_6/ptodata/1/paa/US101.COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US102.COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US60.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2845	100.0	551	PCT-US02-17456-38
2	2845	100.0	551	Sequence 38, Appl
3	2845	100.0	551	Sequence 1, Appl
4	2845	100.0	551	Sequence 1, Appl
5	2845	100.0	551	Sequence 37, Appl
6	2845	100.0	551	Sequence 1642, Ap
7	2845	100.0	551	Sequence 22, Appl

7	2470	86.8	553	19	US-09-521-195B-22	Sequence 22, Appl
8	2454.5	86.3	616	27	US-60-230-445-1548	Sequence 1548, Ap
9	2247	79.0	527	27	US-60-230-445-1385	Sequence 1385, Ap
10	2218	78.0	557	1	PCT-US01-08631-33308	Sequence 33388, A
11	2218	78.0	557	1	PCT-US02-17382-202	Sequence 202, Appl
12	2218	78.0	557	1	PCT-US02-17456-39	Sequence 39, Appl
13	2218	78.0	557	1	PCT-US02-17456-40	Sequence 40, Appl
14	2218	78.0	557	19	US-09-521-195B-3	Sequence 3, Appl
15	2218	78.0	557	19	US-09-521-195B-3	Sequence 3, Appl
16	2218	78.0	557	21	US-09-798-743A-1	Sequence 1, Appl
17	2218	78.0	557	21	US-09-798-743A-1	Sequence 27, Appl
18	2164	76.1	557	19	US-09-521-195B-27	Sequence 27, Appl
19	2164	76.1	557	21	US-09-798-743A-3	Sequence 3, Appl
20	2164	76.1	557	21	US-09-798-743A-3	Sequence 3, Appl
21	2164	76.1	557	21	US-09-798-743A-3	Sequence 297, Appl
22	1955	68.7	400	27	US-60-258-275-297	Sequence 297, Appl
23	1582	55.6	498	27	US-60-230-445-1504	Sequence 1504, Ap
24	1557	54.7	410	27	US-60-230-445-1504	Sequence 1529, A
25	857	30.1	548	20	US-09-614-150-13629	Sequence 517, Appl
26	857	30.1	548	27	US-60-167-245-517	Sequence 13670, A
27	857	30.1	548	27	US-60-167-245-517	Sequence 153, Appl
28	857	30.1	548	27	US-60-219-005-153	Sequence 2414, A
29	857	30.1	548	21	US-09-791-537-21414	Sequence 24599, A
30	852	29.9	567	27	US-60-173-464-24599	Sequence 31854, A
31	821	28.8	567	20	US-09-614-150-31854	Sequence 31426, A
32	819	28.8	567	27	US-60-191-637-31426	Sequence 24934, A
33	819	28.8	567	27	US-60-191-637-31426	Sequence 331, Appl
34	801	28.2	518	27	US-60-145-989-331	Sequence 1029, Appl
35	797.5	28.0	577	1	PCT-US01-04098A-1029	Sequence 9282, Appl
36	773.5	27.2	561	20	US-09-614-150-9282	Sequence 9342, Appl
37	773.5	27.2	561	27	US-60-167-217-9342	Sequence 9311, Appl
38	773.5	27.2	561	27	US-60-191-637-9311	Sequence 2997, Appl
39	773.5	27.2	561	27	PCT-US01-04098A-2997	Sequence 105, Appl
40	748.5	26.3	555	25	US-10-177-488-105	Sequence 1313, Appl
41	704	24.7	555	1	PCT-US01-04098A-1913	Sequence 34, Appl
42	703	24.7	555	1	PCT-US02-17456-34	Sequence 35, Appl
43	703	24.7	555	1	PCT-US02-17456-35	Sequence 104, Appl
44	703	24.7	555	1	PCT-US02-17456-35	
45	703	24.7	555	25	US-10-177-488-104	

#### ALIGNMENTS

RESULT 1  
PCT-US02-17456-38  
Sequence 38, Application PC/TUS0217456  
GENERAL INFORMATION:  
APPLICANT: EXELIXIS, INC.  
FILE REFERENCE: SLC22AS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
CURRENT FILING DATE: 2002-06-03  
CURRENT APPLICATION NUMBER: PCT/US02/17456  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/296,076  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/328,605  
PRIOR FILING DATE: 2001-02-15  
PRIOR APPLICATION NUMBER: US 60/357,253  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 38  
LENGTH: 551  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-17456-38

Query Match 100.0%; Score 2845; DB 1; Length 551;  
Best Local Similarity 100.0%; Pred. No. 2.3e-257;  
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 AMRNSVPLRLRGREVPHSCSRYLATIANFSALGLEPGRVDJGOLQESCLDGMWFS 120
Oy 121 QDYVLSVTVMNLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180
Db 121 QDYVLSVTVMNLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180
Oy 121 QDYVLSVTVMNLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180
Db 121 QDYVLSVTVMNLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180
Oy 181 TGFSFQIIFSIEMEMFTVLFVIVGMQISNYVAALITGTEILGKSVRIIFSTLGCCTEFA 240
Db 181 TGFSFQIIFSIEMEMFTVLFVIVGMQISNYVAALITGTEILGKSVRIIFSTLGCCTEFA 240
Oy 241 VGYMLPLFAFYFRDMRMMLLALTVPGLVCPVLMWFIPESPRLISQRRFRAEDIIQKA 300
Db 241 VGYMLPLFAFYFRDMRMMLLALTVPGLVCPVLMWFIPESPRLISQRRFRAEDIIQKA 300
Oy 301 AKNNNTAVPAVIDSDVEELNPLKQOKAFILDFRTNINAIKMTIMSLMLTSGVFALS 360
Db 301 AKNNNTAVPAVIDSDVEELNPLKQOKAFILDFRTNINAIKMTIMSLMLTSGVFALS 360
Oy 361 LDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRTYIIAVALFPGGVLLFTQVLPV 420
Db 361 LDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRTYIIAVALFPGGVLLFTQVLPV 420
Oy 421 DYFFLSIGVLMGKFGITSAFSLMYETAELVPTLVRNAVGVTSASRVSIIAPFVY 480
Db 421 DYFFLSIGVLMGKFGITSAFSLMYETAELVPTLVRNAVGVTSASRVSIIAPFVY 480
Oy 481 LGAVNRMPLPYIVMGSILVLIGITLFFPSLGMTLPETLEQOKKWFERSGKTRDSMET 540
Db 481 LGAVNRMPLPYIVMGSILVLIGITLFFPSLGMTLPETLEQOKKWFERSGKTRDSMET 540
Oy 541 EENPKVLTIAF 551
Db 541 EENPKVLTIAF 551

RESULT 2
US-09-521-195-1
: Sequence 1, Application US/09521195
: GENERAL INFORMATION:
: APPLICANT: Nezu, Jun-ichi
: TITLE OF INVENTION: TRANSPORTER GENES
: FILE REFERENCE: 06501-057001
: CURRENT APPLICATION NUMBER: US/09/521,195
: CURRENT FILING DATE: 2000-03-07
: PRIOR APPLICATION NUMBER: JP 10/156660
: PRIOR FILING DATE: 1998-05-20
: PRIOR APPLICATION NUMBER: JP 9/260972
: PRIOR FILING DATE: 1997-09-08
: PRIOR APPLICATION NUMBER: PCT/JP98/04009
: PRIOR FILING DATE: 1998-09-07
: NUMBER OF SEQ ID NOS: 32
: SEQ ID NO 1
: LENGTH: 551
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-521-195-1

Query Match 100.0%; Score 2845; DB 19; Length 551;
Best Local Similarity 100.0%; Pred. No. 2,3e-257;
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 QDYVLSVTVMNLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180
Oy 181 TGFSFQIIFSIEMEMFTVLFVIVGMQISNYVAALITGTEILGKSVRIIFSTLGCCTEFA 240
Db 181 TGFSFQIIFSIEMEMFTVLFVIVGMQISNYVAALITGTEILGKSVRIIFSTLGCCTEFA 240
Oy 241 VGYMLPLFAFYFRDMRMMLLALTVPGLVCPVLMWFIPESPRLISQRRFRAEDIIQKA 300
Db 241 VGYMLPLFAFYFRDMRMMLLALTVPGLVCPVLMWFIPESPRLISQRRFRAEDIIQKA 300
Oy 301 AKNNNTAVPAVIDSDVEELNPLKQOKAFILDFRTNINAIKMTIMSLMLTSGVFALS 360
Db 301 AKNNNTAVPAVIDSDVEELNPLKQOKAFILDFRTNINAIKMTIMSLMLTSGVFALS 360
Oy 361 LDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRTYIIAVALFPGGVLLFTQVLPV 420
Db 361 LDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRTYIIAVALFPGGVLLFTQVLPV 420
Oy 421 DYFFLSIGVLMGKFGITSAFSLMYETAELVPTLVRNAVGVTSASRVSIIAPFVY 480
Db 421 DYFFLSIGVLMGKFGITSAFSLMYETAELVPTLVRNAVGVTSASRVSIIAPFVY 480
Oy 481 LGAVNRMPLPYIVMGSILVLIGITLFFPSLGMTLPETLEQOKKWFERSGKTRDSMET 540
Db 481 LGAVNRMPLPYIVMGSILVLIGITLFFPSLGMTLPETLEQOKKWFERSGKTRDSMET 540
Oy 541 EENPKVLTIAF 551
Db 541 EENPKVLTIAF 551

RESULT 3
US-09-521-195b-1
: Sequence 1, Application US/09521195b
: GENERAL INFORMATION:
: APPLICANT: Nezu, Jun-ichi
: TITLE OF INVENTION: TRANSPORTER GENES
: FILE REFERENCE: 06501-057001
: CURRENT APPLICATION NUMBER: US/09/521,195b
: CURRENT FILING DATE: 2000-03-07
: PRIOR APPLICATION NUMBER: JP 10/156660
: PRIOR FILING DATE: 1998-05-20
: PRIOR APPLICATION NUMBER: JP 9/260972
: PRIOR FILING DATE: 1997-09-08
: PRIOR APPLICATION NUMBER: PCT/JP98/04009
: PRIOR FILING DATE: 1998-09-07
: NUMBER OF SEQ ID NOS: 33
: SEQ ID NO 1
: LENGTH: 551
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-521-195b-1

Query Match 100.0%; Score 2845; DB 19; Length 551;
Best Local Similarity 100.0%; Pred. No. 2,3e-257;
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	241	VGMYLLPEFAFVIRDMRMILLATVPGLVCPLWFIIPESPRLMISORPREAEDIIOKA	300
Db	241	VGMYLLPEFAFVIRDMRMILLATVPGLVCPLWFIIPESPRLMISORPREAEDIIOKA	300
QY	301	AKMNNTAVPAVIFDSVEELNPLKOOKAFILDLFETRNAIMTJMSLLMLTISVGFALS	360
Db	301	AKMNNTAVPAVIFDSVEELNPLKOOKAFILDLFETRNAIMTJMSLLMLTISVGFALS	360
QY	361	LDAPNHNHGAIVNCLSLALIEIPATITAMLLRFLPRYITIAALFEMGGVLLFIQLVPY	420
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QY	421	DYFYLSTIGLWMLGKFGITSAFSMLYVFAELYPVLVRNMAVGVSTASRGSITIAPEFYV	480
Db	421	DYFYLSTIGLWMLGKFGITSAFSMLYVFAELYPVLVRNMAVGVSTASRGSITIAPEFYV	480
QY	481	LGATNRMPLPYIMGSLITVLIGITFLFEPESIGMTLPETLEOMOKVKKFRSGKKTROSMET	540
Db	481	LGATNRMPLPYIMGSLITVLIGITFLFEPESIGMTLPETLEOMOKVKKFRSGKKTROSMET	540
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Db	541	EENPKVLITAF 551	

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PCT-US02-17456-37
RESULT 4
PCT-US02-17456-37
Sequence 37, Application PC/TUS0217456
GENERAL INFORMATION:
APPLICANT: EXPLIITS, INC.
TITLE OF INVENTION: SLIC22AS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-086C-PC
CURRENT APPLICATION NUMBER: PCT/US02/17456
PRIOR FILING DATE: 2002-06-03
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 551
TYPE: PRF
ORGANISM: Homo sapiens
PCT-US02-17456-37
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Query Match	99.6%;	Score 2833;	DB 1;	Length 551;
Best Local Similarity	99.6%;	Pred. NO. 3.1e-256;		
Matches 549;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

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Db	1	MRDDEVIAFAGEMCPPORLIFELLASIIIPGFGMGSAVFLAGPPEHCRCVDAANLSS	60
QY	61	AMRNNSVPLRLDREVPDHSCSRYLATIANFSALGLEBDYDGLQEQESCIDGWEFS	120
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QY	121	QDVYISTVVTENNLCEDNMKVPILTSLFEVGLVIGSFSGQLSDRFGRKNLFFATMAAQ	180
Db	121	QDVYISTVVTENNLCEDNMKVPILTSLFEVGLVIGSFSGQLSDRFGRKNLFFATMAAQ	180
QY	181	TGFSFLQIFSISSMEMEFVLFTVVGGOISNYYVAELIGLEIIGKSAVRIIFSTLYGCTFFA	240
Db	181	TGFSFLQIFSISSMEMEFVLFTVVGGOISNYYVAELIGLEIIGKSAVRIIFSTLYGCTFFA	240
QY	241	VGYLMLPLFAFIIDRMRLILATVPGVLCVPLMWFIPBSPKWLISORRFREAEDIIQQA	300

Db	241	VGMLLPLFAFYELRQMRMLLATVPGVLCVPLWMEIPESPRMLISQRRREEDITQKA	300
QY	301	AKANNNAVPAVYFDSEELNPLKOKAPILDLFRNRNAITMISLLMLTSGVFAAS	360
Db	301	AKANNNAVPAVYFDSEELNPLKOKAPILDLFRNRNAITMISLLMLTSGVFAAS	360
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Db	361	LDAPNPHGDVYLCNCFSALEIEIPATYTMLLRTLPRIIAAVALFWGGVLLFIQHPV	420
QY	421	DYFELSIGVLMGKFQITSAFSMLYVFAELYPILVRNMAVGVTSTASRSGSIAPFVY	480
Db	421	DYFELSIGVLMGKFQITSAFSMLYVFAELYPILVRNMAVGVTSTASRSGSIAPFVY	480
QY	481	LGAYNRMLPTIVWGSITVLIGITLFFPESJGMLPELLEOMOKVKKFRSGKTRDSMET	540
Db	481	LGAYNRMLPTIVWGSITVLIGITLFFPESJGMLPELLEOMOKVKKFRSGKTRDSMET	540
QY	541	EENPKVLTIAF 551	
Db	541	EENPKVLTIAF 551	

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RESULT 5
US-60-230-445-1642
; Sequence 1642, Application US/60230445
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000765
; CURRENT APPLICATION NUMBER: US/60/230,445
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 3051
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1642
; LENGTH: 588
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(588)
; OTHER INFORMATION: xaa = Any Amino Acid
US-60-230-445-1642

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query Match	90.7%;	Score 2580.5;	DB 27;	Length 588;
Best Local Similarity	87.6%;	Pred. No. 1.7e-232;		
Matches 514;	Conservative 2;	Mismatches 10;	Indels 61;	Gaps 2

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Db      1 MRDDEVIAIPLGEMGPORLIFELLASITIPNCFNMSVFLAGTPEHRCVPPAANLSS 60
QY      61 AMRNNSVPLRLRGREVPHSCSRYRIATIANFSALEBPGRVDYLGOLBQESCLDGEWFS 120
Db      61 AMRNNSVPLRLRGREVPHSCSRYRIATIANFSALEBPGRVDYLGOLBQESCLDGEWFS 120
QY      121 ODVLSITVYME-----133
Db      121 QDVVLSITVYMEHKKNGSSITLGTYGQENTYLSPISEFGRATTAHQECQPMPLPHPSLSLS 180
QY      132 -----WNLVCDNNKVB/LTTSLEFVGVLLGSEFYSGOLSDFGRKNVLEPATMAVQIGSEFL 186
Db      131 SKPQKMLVCDNNKVB/LTTSLEFVGVLLGSEFYSGOLSDFGRKNVLEPATMAVQIGSEFL 240
QY      167 QIFSIWSEMTVLEFVIWGMQOISNYVAFLTGTELLGKSVRIIFSTLGVCFPFAVGWML 244
Db      241 QIFSIWSEMTVLEFVIWGMQOISNYVAFLTGTELLGKSVRIIFSTLGVCFPFAVGWML 300
QY      247 PLFAFYLRDWMMLLALTTPGVLCVPLWMTIPSPWML-----SQRREPADITQK 299

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QY 300 AAKNNNTAVPAVIFDSVEEENPLKOOKAFITLDFPRNRNIAIMTISLLMLMTSVGYFAL 359  
Db 361 AAKNNNTAVPAVIFDSVEEENPLKOOKAFITLDFPRNRNIAIMTISLLMLMTSVGYFAL 420  
QY 360 SLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 419  
Db 421 SLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 480  
QY 420 VDYFFLSIGLVMGKRGITSAFSAFMLYVFAELPVLVRMAVGVSTASRGSIITAPYV 479  
Db 481 VDYFFLSIGLVMGKRGITSAFSAFMLYVFAELPVLVRMAVGVSTASRGSIITAPYV 540  
QY 480 YLGAYNRLPYIYVGSITLVIGITLFFPESIGMTLPETLEOKOKYK 526  
Db 541 YLGAYNRLPYIYVGSITLVIGITLFFPESIGMTLPETLEOKOKYK 587  
RESULT 6  
US-09-521-195-22  
Sequence 22, Application US/09521195  
GENERAL INFORMATION:  
APPLICANT: Nezu, Jun-ichi  
FILE REFERENCE: 06501-057001  
TITLE OF INVENTION: TRANSPORTER GENES  
CURRENT APPLICATION NUMBER: US/09/521,195  
CURRENT FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: JP 10/156660  
PRIOR FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: JP 9/260972  
PRIOR FILING DATE: 1997-09-08  
PRIOR APPLICATION NUMBER: PCT/JP98/04009  
PRIOR FILING DATE: 1998-09-07  
NUMBER OF SEQ ID NOS: 32  
SEQ ID NO 22  
LENGTH: 553  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-521-195-22  
Query Match 86.8%; Score 2470; DB 19; Length 553;  
Best Local Similarity 84.6%; Pred. No. 3,6e-222;  
Matches 468; Conservative 39; Mismatches 44; Indels 2; Gaps 1;  
QY 1 MRDYDEVIAFLGEMGFORLIFELLASIIIPNGFNGMSVFLAGTPBHRCPVDAANLSS 60  
Db 1 MRDYDEVIAFLGEMGFORLIFELLASIIIPNGFNGMSVFLAGTPBHRCPVDAANLSS 60  
QY 61 AARNNSVPLRLDGRVPHSCRRYRLATIANFSALGLEPGRVDYLGQLEBESCLDGMERS 120  
Db 61 SMRNHSIPLETKDGROVPQSCRRYRLATIANFSAMGLEPQDQVDLEQLEBESCLDGMERYD 120  
QY 121 QDYYLSTVYTEMNLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRGRKNVLFATMAVQ 180  
Db 121 KQIFLSTVTEMNLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRGRKNVLFATMAVQ 180  
QY 181 TGFSEFQIFSTWMEFTVLAIVGQGISNYVAFLIGTELKSVRIIFSTIGVCTFFA 240  
Db 181 TGFSEFQIFSTWMEFTVLAIVGQGISNYVAFLIGTELKSVRIIFSTIGVCTFFA 240  
QY 241 VGYMLPLFAFIRDMRMLLALTVPGVLCVPLMWFIPESPRLISORRFAEDIIQK 300  
Db 241 IGYVPLPLFAFIRDMRMLLALTVPGVLCVPLMWFIPESPRLISORRFAEDIIQK 300  
QY 301 AKNNNTAVPAVIFDSVE--ELNPLKOOKAFITLDFRTNRNIAIMTISLLMLMTSVGYFA 358  
Db 301 AKNNNTAVPAVIFDSVEEENPLKOOKAFITLDFRTNRNIAIMTISLLMLMTSVGYFA 360  
QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 418  
Db 361 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 420

QY 419 PVDYFFLSIGLVMGKRGITSAFSAFMLYVFAELPVLVRMAVGVSTASRGSIITAPYF 478  
Db 421 PEDYNFVSIGLVMGKRGITSAFSAFMLYVFAELPVLVRMAVGVSTASRGSIITAPYF 480  
QY 479 YVIGAYNRLPYIYVGSITLVIGITLFFPESIGMTLPETLEOKOKYKVPFSGKTRBSM 538  
Db 481 YVIGAYNRLPYIYVGSITLVIGITLFFPESIGMTLPETLEOKOKYKVPFSGKTRBSM 540  
QY 539 ETEENPKVLTIAF 551  
Db 541 DREESPKVLTIAF 553  
RESULT 7  
US-09-521-195b-22  
Sequence 22, Application US/09521195b  
GENERAL INFORMATION:  
APPLICANT: Nezu, Jun-ichi  
FILE REFERENCE: 06501-057001  
TITLE OF INVENTION: TRANSPORTER GENES  
CURRENT APPLICATION NUMBER: US/09/521,195b  
CURRENT FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: JP 10/156660  
PRIOR FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: JP 9/260972  
PRIOR FILING DATE: 1997-09-08  
PRIOR APPLICATION NUMBER: PCT/JP98/04009  
PRIOR FILING DATE: 1998-09-07  
NUMBER OF SEQ ID NOS: 33  
SEQ ID NO 22  
LENGTH: 553  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-521-195b-22  
Query Match 86.8%; Score 2470; DB 19; Length 553;  
Best Local Similarity 84.6%; Pred. No. 3,6e-222;  
Matches 468; Conservative 39; Mismatches 44; Indels 2; Gaps 1;  
QY 1 MRDYDEVIAFLGEMGFORLIFELLASIIIPNGFNGMSVFLAGTPBHRCPVDAANLSS 60  
Db 1 MRDYDEVIAFLGEMGFORLIFELLASIIIPNGFNGMSVFLAGTPBHRCPVDAANLSS 60  
QY 61 AARNNSVPLRLDGRVPHSCRRYRLATIANFSALGLEPGRVDYLGQLEBESCLDGMERS 120  
Db 61 SMRNHSIPLETKDGROVPQSCRRYRLATIANFSAMGLEPQDQVDLEQLEBESCLDGMERYD 120  
QY 121 QDYYLSTVYTEMNLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRGRKNVLFATMAVQ 180  
Db 121 KQIFLSTVTEMNLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRGRKNVLFATMAVQ 180  
QY 181 TGFSEFQIFSTWMEFTVLAIVGQGISNYVAFLIGTELKSVRIIFSTIGVCTFFA 240  
Db 181 TGFSEFQIFSTWMEFTVLAIVGQGISNYVAFLIGTELKSVRIIFSTIGVCTFFA 240  
QY 241 VGYMLPLFAFIRDMRMLLALTVPGVLCVPLMWFIPESPRLISORRFAEDIIQK 300  
Db 241 IGYVPLPLFAFIRDMRMLLALTVPGVLCVPLMWFIPESPRLISORRFAEDIIQK 300  
QY 301 AKNNNTAVPAVIFDSVE--ELNPLKOOKAFITLDFRTNRNIAIMTISLLMLMTSVGYFA 358  
Db 301 AKNNNTAVPAVIFDSVEEENPLKOOKAFITLDFRTNRNIAIMTISLLMLMTSVGYFA 360  
QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 418  
Db 361 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 420  
QY 419 PVDYFFLSIGLVMGKRGITSAFSAFMLYVFAELPVLVRMAVGVSTASRGSIITAPYF 478  
Db 421 PEDYNFVSIGLVMGKRGITSAFSAFMLYVFAELPVLVRMAVGVSTASRGSIITAPYF 480



PCT-US01-08631-33388

; Sequence 33388, Application PC/TUS0108631

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 21272-049

; CURRENT APPLICATION NUMBER: PCT/US01/08631

; PRIORITY FILING DATE: 2001-03-30

; PRIORITY FILING DATE: 2000-03-31

; PRIORITY FILING DATE: 2000-03-31

; PRIORITY FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 33388

; LENGTH: 557

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (428)..(478)

; OTHER INFORMATION: Sugar transport proteins domain identified by eMATRIX,

; OTHER INFORMATION: accession number BL00216b, p-value=4.375e-11, raw score of 27.64

; NAME/KEY: DOMAIN

; LOCATION: (108)..(525)

; OTHER INFORMATION: Sugar (and other) transporter domain identified by Pfam,

; OTHER INFORMATION: accession name sugat\_tr, E-value=5.6e-08, Pfam score of 32.9

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RESULT 11

PCT-US02-17382-202

; Sequence 202, Application PC/TUS0217382

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX02-062

; CURRENT APPLICATION NUMBER: PCT/US02/17382

; PRIORITY FILING DATE: 2002-06-05

; PRIORITY FILING DATE: 2002-06-05

; PRIORITY FILING DATE: 2001-06-05

; PRIORITY FILING DATE: 2001-10-10

; PRIORITY FILING DATE: 2001-10-10

; PRIORITY FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 234

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 202

; LENGTH: 557

; TYPE: PRT

; ORGANISM: Homo sapiens

; PCT-US02-17382-202

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RESULT 12

PCT-US02-17456-39

; Sequence 39, Application PC/TUS0217456

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX02-062

; CURRENT APPLICATION NUMBER: PCT/US02/17382

; PRIORITY FILING DATE: 2002-06-05

; PRIORITY FILING DATE: 2002-06-05

; PRIORITY FILING DATE: 2001-06-05

; PRIORITY FILING DATE: 2001-10-10

; PRIORITY FILING DATE: 2001-10-10

; PRIORITY FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 234

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 202

; LENGTH: 557

; TYPE: PRT

; ORGANISM: Homo sapiens

; PCT-US02-17382-202

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; PRIOR APPLICATION NUMBER: PCT/JP98/04009  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 32  
; SEQ ID NO 3  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-521-195-3

Query Match 78.0%; Score 2218; DB 19; Length 557;  
Best Local Similarity 75.9%; Pred. No. 1.6e-198;  
Matches 423; Conservative 57; Mismatches 71; Indels 6; Gaps 3;

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DB 1 MRDYEVIAFLGEMGFQRLIFLLSASIIIPNGFNGMSVFLAGTPHRCRVPDAANLSS 60
QY 61 AMRNHVPRLRDRGVPVPHSCRYRATIANFSALEPGRDVDLQGLEQESCLDGEFS 120
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DB 121 ODVYLSIVTEMNLVCEDMKAPLTLSLFFVGVLLGSFVSGQLSDRFRKKNVLFATMAVQ 180
QY 181 TGFSLQIFISISMEFTVLFYVGMQISNYVAFLIGTELLGKSVRIIFSTLGVCYFEA 240
DB 181 TGFSLQIFISISMEFTVLFYVGMQISNYVAFLIGTELLGKSVRIIFSTLGVCYFEA 240
QY 241 VGYMLPLFAFIRDMRMILLATVPGVLCVPLMFIPESPRMLISORFREAEEDIIQKA 300
DB 241 VGYMLPLFAFIRDMRMILLATVPGVLCVPLMFIPESPRMLISORFREAEEDIIQKA 300
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DB 301 AKANNTAVPAVIFD--SVEELNPLKQOKAFIIDLFRNTIAINTMSLLMLLSVGYFA 358
QY 359 LSLDAPNLGDAYLNCFELALIEIPAYITAMLLRLTPRYITIAVLFPMGGLVFIOLV 418
DB 359 LSLDAPNLGDAYLNCFELALIEIPAYITAMLLRLTPRYITIAVLFPMGGLVFIOLV 418
QY 419 PVDYFELSIGLVMLGFGITSAFSLMYFETAEIPLTVRNMAVGVTSASRYGSIITAYF 478
DB 419 PVDYFELSIGLVMLGFGITSAFSLMYFETAEIPLTVRNMAVGVTSASRYGSIITAYF 478
QY 479 VYLGAVNRLPYIYVMSLTVLIGITLFFPESLGMTLPETLEQMKVYWRSGK---KTR 535
DB 479 VYLGAVNRLPYIYVMSLTVLIGITLFFPESLGMTLPETLEQMKVYWRSGK---KTR 535
QY 536 DSMETENPKVL--ITAF 551
DB 536 DSMETENPKVL--ITAF 551
QY 541 MKDQGERPTIIKSTAF 557
DB 541 MKDQGERPTIIKSTAF 557
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RESULT 15  
US-09-521-195b-3  
; Sequence 3, Application US/09521195b  
; GENERAL INFORMATION:  
; APPLICANT: Nezu, Jun-ichi  
; TITLE OF INVENTION: TRANSPORTER GENES  
; FILE REFERENCE: 06501-057001  
; CURRENT APPLICATION NUMBER: US/09/521.195b  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: JP 10/156660  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: JP 9/260972  
; PRIOR FILING DATE: 1997-09-08  
; PRIOR APPLICATION NUMBER: PCT/JP98/04009  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 33  
; SEQ ID NO 3  
; LENGTH: 557

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-521-195b-3

Query Match 78.0%; Score 2218; DB 19; Length 557;  
Best Local Similarity 75.9%; Pred. No. 1.6e-198;  
Matches 423; Conservative 57; Mismatches 71; Indels 6; Gaps 3;

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QY 1 MRDYEVIAFLGEMGFQRLIFLLSASIIIPNGFNGMSVFLAGTPHRCRVPDAANLSS 60
DB 1 MRDYEVIAFLGEMGFQRLIFLLSASIIIPNGFNGMSVFLAGTPHRCRVPDAANLSS 60
QY 61 AMRNHVPRLRDRGVPVPHSCRYRATIANFSALEPGRDVDLQGLEQESCLDGEFS 120
DB 61 AMRNHVPRLRDRGVPVPHSCRYRATIANFSALEPGRDVDLQGLEQESCLDGEFS 120
QY 121 ODVYLSIVTEMNLVCEDMKAPLTLSLFFVGVLLGSFVSGQLSDRFRKKNVLFATMAVQ 180
DB 121 ODVYLSIVTEMNLVCEDMKAPLTLSLFFVGVLLGSFVSGQLSDRFRKKNVLFATMAVQ 180
QY 181 TGFSLQIFISISMEFTVLFYVGMQISNYVAFLIGTELLGKSVRIIFSTLGVCYFEA 240
DB 181 TGFSLQIFISISMEFTVLFYVGMQISNYVAFLIGTELLGKSVRIIFSTLGVCYFEA 240
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DB 241 VGYMLPLFAFIRDMRMILLATVPGVLCVPLMFIPESPRMLISORFREAEEDIIQKA 300
QY 301 AKANNTAVPAVIFD--SVEELNPLKQOKAFIIDLFRNTIAINTMSLLMLLSVGYFA 358
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DB 359 LSLDAPNLGDAYLNCFELALIEIPAYITAMLLRLTPRYITIAVLFPMGGLVFIOLV 418
QY 419 PVDYFELSIGLVMLGFGITSAFSLMYFETAEIPLTVRNMAVGVTSASRYGSIITAYF 478
DB 419 PVDYFELSIGLVMLGFGITSAFSLMYFETAEIPLTVRNMAVGVTSASRYGSIITAYF 478
QY 479 VYLGAVNRLPYIYVMSLTVLIGITLFFPESLGMTLPETLEQMKVYWRSGK---KTR 535
DB 479 VYLGAVNRLPYIYVMSLTVLIGITLFFPESLGMTLPETLEQMKVYWRSGK---KTR 535
QY 536 DSMETENPKVL--ITAF 551
DB 536 DSMETENPKVL--ITAF 551
QY 541 MKDQGERPTIIKSTAF 557
DB 541 MKDQGERPTIIKSTAF 557
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Search completed: July 3, 2003, 12:41:39  
Job time : 152 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2003, 12:37:45 ; Search time 25 Seconds  
(without alignments)  
2534.444 Million cell updates/sec

Title: US-09-521-195B-1

Perfect score: 2845  
Sequence: 1 MRDYDEVIAFLGEMGPPQRL.....KTRDSMETENKVLITAF 551

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 440863 seqs, 114992915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PTCT\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB pep:\*  
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14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2164	76.1	557	10	US-09-798-743A-3
3	691.5	24.3	556	9	US-09-284-320-83
4	685.5	24.1	554	9	US-09-284-320-5
5	654.5	23.0	547	9	US-10-155-891-2
6	641	22.5	476	9	US-10-155-891-4
7	625.5	22.0	553	9	US-10-095-139-5
8	599	21.1	553	9	US-10-095-139-17
9	586	20.6	550	9	US-10-086-816A-2
10	564	19.8	550	9	US-10-095-139-16
11	564	19.8	550	9	US-10-339-513-2
12	398	14.0	572	10	US-09-919-781-2
13	303.5	10.7	448	9	US-09-738-626-6795
14	280	9.8	486	10	US-09-860-232A-7
15	276.5	9.7	488	9	US-10-170-528-5
16	276.5	9.7	488	9	US-10-062-960B-4
17	276.5	9.7	488	9	US-10-162-012-46
18	276.5	9.7	488	9	US-10-144-624-4
19	276.5	9.7	488	12	US-10-094-059-4

20	275.5	9.7	487	9	US-10-095-139-14	Sequence 14, Appl
21	275.5	9.7	487	9	US-10-156-239-27	Sequence 27, Appl
22	275.5	9.7	487	9	US-10-199-485-27	Sequence 27, Appl
23	275.5	9.7	487	10	US-09-795-693-27	Sequence 2, Appl
24	267	9.4	520	9	US-10-000-273-2	Sequence 20, Appl
25	266.5	9.4	535	9	US-10-156-239-20	Sequence 20, Appl
26	266.5	9.4	535	9	US-10-199-485-20	Sequence 20, Appl
27	266.5	9.4	535	10	US-09-795-693-20	Sequence 20, Appl
28	247	8.7	530	9	US-09-991-936-1902	Sequence 1902, Ap
29	246.5	8.7	490	9	US-10-128-714-8149	Sequence 8149, Ap
30	244.5	8.6	727	9	US-10-170-528-4	Sequence 4, Appl
31	244.5	8.6	727	10	US-09-822-246-4	Sequence 4, Appl
32	243	8.5	431	9	US-09-738-626-6697	Sequence 4697, Ap
33	240.5	8.5	469	9	US-10-156-761-9834	Sequence 9834, Ap
34	239	8.4	480	9	US-10-176-847-76	Sequence 76, Appl
35	237.5	8.3	727	10	US-09-822-246-2	Sequence 2, Appl
36	237	8.3	474	9	US-10-128-714-8149	Sequence 3149, Ap
37	234.5	8.2	494	9	US-09-981-947A-5	Sequence 5, Appl
38	234	8.2	405	10	US-09-972-724-5	Sequence 36, Appl
39	234	8.2	553	9	US-10-051-909-16	Sequence 48, Appl
40	233	8.2	501	10	US-09-778-927A-48	Sequence 47, Appl
41	227	8.0	471	10	US-09-778-927A-47	Sequence 5079, Ap
42	224.5	7.9	451	10	US-09-815-242-5079	Sequence 160, Ap
43	219	7.7	742	9	US-09-374-046A-160	Sequence 10, Appl
44	216	7.6	493	9	US-09-981-947A-10	Sequence 22, Appl
45	216	7.6	510	9	US-10-051-902-22	

#### ALIGNMENTS

```

RESULT 1
US-09-798-743A-1
; Sequence 1, Application US/09798743A
; Patent No. US2002009903A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: SYSTEMIC CARNITINE DEFICIENCY GENE AND USES THEREOF
; FILE REFERENCE: 06501-073001
; CURRENT APPLICATION NUMBER: US/09/798,743A
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/JP99/04853
; PRIOR FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: JP 10-252683
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-743A-1

Query Match      78.0%; Score 2218; DB 10; Length 557;
Best Local Similarity 75.9%; Pred. No. 2.4e-182;
Matches 423; Conservative 57; Mismatches 71; Indels 6; Gaps 3;

OY      1 MRDYDEVIAFLGEMGPPQRLIFPFLISAIITNGNGMSVFLACTPBRKRVDAANLSS 60
||||| 1 MRDYDEVIAFLGEMGPPQRLIFPFLISAIITNGNGMSVFLACTPBRKRVDAANLSS 60
||||| 1 MRDYDEVIAFLGEMGPPQRLIFPFLISAIITNGNGMSVFLACTPBRKRVDAANLSS 60
||||| 1 MRDYDEVIAFLGEMGPPQRLIFPFLISAIITNGNGMSVFLACTPBRKRVDAANLSS 60
DB      1 MRDYDEVIAFLGEMGPPQRLIFPFLISAIITNGNGMSVFLACTPBRKRVDAANLSS 60
||||| 1 MRDYDEVIAFLGEMGPPQRLIFPFLISAIITNGNGMSVFLACTPBRKRVDAANLSS 60
OY      61 AMRNNVPLRLDGEVPHSCSRVRLATIANFSALGLEPGADVVLGOLDESCIDGMEFS 120
||||| 61 AMRNNVPLRLDGEVPHSCSRVRLATIANFSALGLEPGADVVLGOLDESCIDGMEFS 120
DB      61 AMRNNVPLRLDGEVPHSCSRVRLATIANFSALGLEPGADVVLGOLDESCIDGMEFS 120
||||| 61 AMRNNVPLRLDGEVPHSCSRVRLATIANFSALGLEPGADVVLGOLDESCIDGMEFS 120
OY      121 ODVYISTVVTENMLCEDNMKVPILTSLEFVGVILGSFVSQSLDRGRNNVLPATMAVO 180
||||| 121 ODVYISTVVTENMLCEDNMKVPILTSLEFVGVILGSFVSQSLDRGRNNVLPATMAVO 180
DB      121 ODVYISTVVTENMLCEDNMKVPILTSLEFVGVILGSFVSQSLDRGRNNVLPATMAVO 180
||||| 121 ODVYISTVVTENMLCEDNMKVPILTSLEFVGVILGSFVSQSLDRGRNNVLPATMAVO 180
OY      181 TGFSFLOIFSIEMKEMETLVYVGMSNVVAFILGTETILGKSVRIITSTLGCVCFFA 240
||||| 181 TGFSFLOIFSIEMKEMETLVYVGMSNVVAFILGTETILGKSVRIITSTLGCVCFFA 240
DB      181 TGFSFLOIFSIEMKEMETLVYVGMSNVVAFILGTETILGKSVRIITSTLGCVCFFA 240
||||| 181 TGFSFLOIFSIEMKEMETLVYVGMSNVVAFILGTETILGKSVRIITSTLGCVCFFA 240

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DB 338 LRTPLMKRHTVILMTIMFSCAVILYOGILMHGATGANLILDFEVSSLSVEFPAPLILVT 397  
OY 392 LRTPLRRTIILAVLFWGGVLLFIQVLVPDYFFLSIGLMLKRGITSAFSLIYFTAE 451  
DB 398 IDRIQIYIPLASNLVYGAACILMIFIPHELMVNTVLACLRMCAITVLOAVCVNML 457  
OY 452 YFTLVNMAVGVTSASRVGSIILAPYFY-LGAYNRMLPYIYMGSLTVLIGITLFFPES 510  
DB 458 YFTLVNMAVGVTSASRVGSIILAPYFY-LGAYNRMLPYIYMGSLTVLIGITLFFPES 510  
OY 511 LGMTLPETLEQOKV 525  
DB 518 KGVLPETLEQENL 532

RESULT 4  
US-09-284-320-5  
; Sequence 5, Application US/09284320  
; Publication No. US20030092175A1  
; GENERAL INFORMATION:  
; APPLICANT: Kato, Seishi et al.  
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs  
; FILE REFERENCE: GIN-6703CPUS  
; CURRENT APPLICATION NUMBER: US/09/284,320  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: JP 8-301429  
; PRIOR FILING DATE: 1996-11-13  
; PRIOR APPLICATION NUMBER: PCI/J97/04056  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 554  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-284-320-5

Query Match  
Best Local Similarity 24.1%; Score 685.5; DB 9; Length 554;  
Matches 190; Conservative 87; Mismatches 229; Indels 69; Gaps 14;

OY 1 MNDYEVIAFLGEMWPFOR--LIFELLASIIIPNGFMGVFLAGTPHRRCRVPPDAN 57  
DB 1 MPTVDILIOVGESEGMFOKAPFLIILCLLSAFAF--ICVGIYVFGPDRHCGSPVAE 57  
OY 58 LSS--AMR-----NNSVPLRLDGRVPHSCSRV-----LATIA-NFSALG 96  
DB 58 LSGRGMSPAELNATVPGLAGPAGAFIAGQCHRYEVDMNQSALSCVDPLASLATNRSHLP 117  
OY 97 LEPGRDVDLGOLEOESCLDGWFEFSODVYLSIVTEEMNLVCEEDNMKVPITTSLEFVGLG 156  
DB 118 LCP-----CQDGMVY--DTFGSSIVTEFNIVCADSKWLDLDFQSLNAGFFEG 162  
OY 157 SFVQSOLSRGRKRVLAITMAVOTGFSEFLQFISIMEMFTVLEVIVMGQISNVYAFI 216  
DB 163 SLGVGYFADRFGRKCLLGTIVLVNVSGLMAFSPNYSMLFRLQGLVSKGNMAGYT 222  
OY 217 LCTELLG-----KSVILFSTLGVCFPAVGVMLLPLFYFIRDMMLLALTVPGVLCVP 272  
DB 223 LITTEVSGSRTVAILYOMA-----FTVGLVALTGLAYALPHMWMQLAVSLPTEFL 277  
OY 273 LMFIFESPRLMISQRREAEEDIIQAKAKNNNTAVPAVI-----FDSVEELNPKOOK 326  
DB 278 YVMCVPESPRMLLSQKRTEAIKIMDHIAQKNGKLPADIKMLSLDEYVETKSP----- 332  
OY 327 ATILDFRTNIAITFISLIMLTSGYFALSIDAPNLHGDAYLNCFLSALIEIPAYI 386  
DB 333 -SFALFRTPLRKRTFLIMLTGFDVLYOGLIIMHGCATSGNITLIDFLYSALVEIPGAF 391  
OY 387 TMLLRTPLRRTIILAVLFWGGVLLFIQVLVPDYFFLSIGLMLKRGITSAFSLIY 446

DB 392 IALITDRVGRITPVANSNLAGAACLMIFISPDLMHNLIIIMCGRMGITIAIOMICL 451  
OY 447 FTALHPPLVNVMAVGVTSASRVGSIILAPYFY-LGAYNRMLPYIYMGSLTVLIGITL 505  
DB 452 VNAELYPFVFNGLVMCCSSICLDIGGITPPIVERLEWQALPILIFAVLGLAAGVT 511  
OY 506 FEPESIGMTLPETLEQOKVWFRSGKTRDSMT 540  
DB 512 LLPETKVALPETMKDLENL-----GRNAKENT 541

RESULT 5  
US-10-155-891-2  
; Sequence 2, Application US/10155891  
; Publication No. US20020193585A1  
; GENERAL INFORMATION:  
; APPLICANT: Walke, D. Wade  
; APPLICANT: Fridde, Carl Johan  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; TITLE OF INVENTION: No. US20020193585A1el Human Transporter Proteins and Polynucle  
; FILE REFERENCE: LEX-0346-USA  
; CURRENT APPLICATION NUMBER: US/10/155, 891  
; PRIOR FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/293,710  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 547  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-155-891-2

Query Match  
Best Local Similarity 32.2%; Score 654.5; DB 9; Length 547;  
Matches 175; Conservative 86; Mismatches 232; Indels 51; Gaps 9;

OY 3 DYDEVIAFLGEMWPFORLIFPLLSAST-IPNGFMGVFLAGTPHRRCRVPPDANISSA 61  
DB 2 EBERAFQAVGCMGYQMYLCFLAVLLQVLVATEALIALVATPSYHM--DLAELD--- 55  
OY 62 WRNSVPLRLDGRVPHSCSRVRLATIANFSALGLEPGRDVDLGOLEQSCLDGWFESQ 121  
DB 56 -----LPMOSHNGSAGEDQAFG--DMLLTANGSETHK 86  
OY 122 DVLIS---IVTEEMNLVCEEDNMKVPITTSLEFVGLLGSFVSQSLDRGRKNVLPATM 177  
DB 87 HVHSSSFSTIASSEMFILANSYKVSAASSFEGVGVYISFGQLSDRGRKNVLTGF 146  
OY 178 AVQGFSEFLQFISIMEMFTVLEVIVMGQISNVYAFIITGLTKGSVAIIISTIGVCT 237  
DB 147 ALDLIFLANSFSSYFPAVTRFLVGMNGMSLAVLLNRCVGAAYMALGSG-GL 205  
OY 238 FFAVGMILPLFAFIFIDRMMLLALTVPGVLCVPLMFIPESPRMLISQRREAEEDII 297  
DB 206 FFAVGIAGVALLGVFIRSMFTIALVNLGTVVFLSLFIPESPRMLYSGRISAEAL 265  
OY 298 OKAKANNNTAVPAVIPDSVEELNPKQOKAFIIDLFTFNIAITMTNSLIMLTSGYF 357  
DB 266 YLIAKRRKRL--KCTFSLTPRANSCRETSFDLFRYVLLGHTLIMFIMFVCSIVY 323  
OY 358 ALSIDAPNLHGDAYLNCFLSALIEIPAYIATMLL--RLPRTIILAVLFWGGVLLFI 415  
DB 324 GLTISAGDLGSIYANALSLGLIETPSYPLCTIYLINOKWFGRRRTLSAFICLGLACLV 383  
OY 416 QLVV-----VDYFISIGLVMKRGITSAFSLIYFTAEIYPTLVNMAVGVTSAS 469  
DB 384 MFLPEKDTGVFAVNVNHSLSLGLKILSAFNIYIYTSLELPIYIRNGLGTCGMEFR 443  
OY 470 VGSIIAPYFYLGAYNRMLPYIYMGSLTVLIGITLFFPESLGMTLPETLEQOKVWFR 529

Db 444 VGGIAPFIPSLKYQVMSLPFIVFGANGLTSGILSLPLETFLSPLLETFSDLYQVSYRR 503  
QY 530 SGKK 533  
Db 504 LGEE 507

RESULT 6  
US-10-155-891-4

; Sequence 4, Application US/10155891  
; Publication No. US20020193585A1  
; GENERAL INFORMATION:  
; APPLICANT: Walke, D. Wade  
; APPLICANT: Friddele, Carl Johan  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; TITLE OF INVENTION: No. US20020193585A1el Human Transporter Proteins and Polynucleoti  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: LEX-0346-USA  
; CURRENT APPLICATION NUMBER: US/10/155,891  
; CURRENT FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/293,710  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 476  
; TYPE: PR  
; ORGANISM: homo sapiens  
US-10-155-891-4

Query Match 22.5%; Score 641; DB 9; Length 476;  
Best Local Similarity 35.3%; Pred. No. 6.5e-47;  
Matches 159; Conservative 73; Mismatches 190; Indels 28; Gaps 6;

QY 92 FSAALGERDVLGLOEJSCLDGWEFSDVLYSTVYEMNLYCEDNKKVPLTSLFVY 151  
Db 7 FOAVG-----EMGYQMTLC-----FLAVLLQWFLIARSRKVSAASSFPS 49  
QY 152 GVLGSEFVSGSLDRFRKKNVLFATMAVQTGFSPQIFSTISWEMFTVLFYVGMQISNV 211  
Db 50 GVEVGVISFGSLDRGRKKNVLYLGFALDLFAIANGFSYSYEFVATRFIVGMNMGMS 109  
QY 212 VVAFLGTETLGSVRIESTLGVCFPAVGYMLPLFAFTRDMRLALITVPGVLCV 271  
Db 110 LVAFVLLNECVGAYMALGSIG-GLFFAVGIAQVALLGYFIRSMRTLAILVMLQGVYF 168  
QY 272 PLWMEFESPRWLTISORPREADITIOKAKMNTAVPAVIFDSVEELNPKQKAFITD 331  
Db 169 LLSLFIPEPRWLTISORPREADITIOKAKMNTAVPAVIFDSVEELNPKQKAFITD 226  
QY 332 LFTRTNIAITMSLLMLTSGVYFALSIDAPNLHGDAYLNCFLSALIEIPAYITAMLL 391  
Db 227 LFRRVLLGHTLLIMFTWCVSLVYGLTSLAGDLGSIYANLALSGLEIPEISYPLCIYL 286  
QY 392 L-RTLPKRTIIVAVLEWGGVLLFQIVP-----VDYFELISGLVMGKREITAFSPM 443  
Db 287 INOKWFGKRTLSAFCLGLACLIWFLPEKRDGVFAVAVNSHSLGKLTISAENI 346  
QY 444 LVYFETALVPTLVNMAVGTSTASRVSITIAFYVLYGAYNRMLEPIYVWGLTIVLIGIF 503  
Db 347 VYITSTELVTVIRNNGLGCSMFNRVGIATFISLKYQVMSLPFIVFGANGLTSGIL 406  
QY 504 TLEFPESLGMTLEPTELOMKVWFRSGKK 533  
Db 407 SLLEPTELNSPLLETFSDLYQVSYRRLEE 436

RESULT 7  
US-10-095-139-5  
; Sequence 5, Application US/10095139  
; Patent No. US20020165357A1  
; GENERAL INFORMATION:

; APPLICANT: Curtis, RORY A.J.  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; TITLE OF INVENTION: 38554, 57301, and 58324, Human Organic  
; TITLE OF INVENTION: Ion Transporters and Uses Therefor  
; FILE REFERENCE: MP101-017P1RM  
; CURRENT APPLICATION NUMBER: US/10/095,139  
; CURRENT FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/275,172  
; PRIOR FILING DATE: 2001-03-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 553  
; TYPE: PR  
; ORGANISM: homo sapiens  
; OTHER INFORMATION: unknown amino acids at 200-202  
; NAME/KEY: VARIANT  
; LOCATION: (1)....(553)  
; OTHER INFORMATION: Xaa - Any Amino Acid  
US-10-095-139-5

Query Match 22.0%; Score 625.5; DB 9; Length 553;  
Best Local Similarity 30.1%; Pred. No. 1.7e-45;  
Matches 165; Conservative 101; Mismatches 235; Indels 47; Gaps 10;

QY 4 VDEVATFLEWGPGRILFFLLSAILNGFNGSVPLAGTPERCRVP-----DAA 56  
Db 3 FSELDLVGGIGRFOVLOTMALMVSIMULQSKLENFSAVPSRCAPLLDNTAQA 62  
QY 57 NLSSAMRNNSVPLRLDQ-REVPHSCSYRL-----ATIANFSALGERDVLG 106  
Db 63 ILGSLPALLAISIPGPBQNPQCRFRPQOMQLDNPNTAFATMSADREP----- 115  
QY 107 QLEQSCLDGWEFSDVLYSTVYEMNLYCEDNKKVPLTSLFVGYLGSFVSGQLSDR 166  
Db 116 -----CVDGWYDRIESTITVAKMNLVCSHALKPMASITVLAGIIVGAACGPASDR 169  
QY 167 FGRKNVL--FATMAVQ--TGSEFQIFSI-SWEMFTVLFYVGMQISNVYAFITGEI 221  
Db 170 FGRRLVLRWSYIQMAVMTAAAFAPAFVYXXRRLLAFHSGAEPG--LLAVMENTAA 227  
QY 222 LKSVRIITFSTLGVCTFPAVGYMLPLFAFTRDMRLALITVPGVLCVLMFIPESP 281  
Db 228 RARPLVMTLNSIG----FSFGHGLTAAVAYGVRDITLQIVSYVEFLCFYSSWLAESA 283  
QY 282 RMLISORPREADITIOKAKMNTAVPAVIFDSVEELNPKQKAFITDLEFRT 335  
Db 284 RMLITTGRLDMLQELMRYAPVINGKAVQDITLPEVLLSAMRELSMGQPPASIGTLLM 343  
QY 336 RNIAITMSLLMLTSGVYFALSIDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTL 395  
Db 344 PCLRRRTCTSLCWPAFTFEGFALDLQALGNSIFLLQMFIGVVDIPAKMGALLLSHL 403  
QY 396 PRRTIIVAVLEWGGVLLFQIVPYDYFELISGLVMGKREITAFSPMLVYFETALV 455  
Db 404 GRPPLTASLLLAGICLANTLVPEHMGALSALAVALGSGVGAFTCTITTYSELPEPTL 463  
QY 456 VNNMAVGTSTASRVSITIAFYVLYGAYNRMLEPIYVWGLTIVLIGIFTEPESLQWTL 515  
Db 464 LKMTAVGIGQMAARAGAILGLPLVRLLVGHGFWMLPLVYGVYVLSGLAALLPFTQSLPL 523  
QY 516 PETLEOMQ 523  
Db 524 PDTIDVQ 531

RESULT 8  
US-10-095-139-17  
; Sequence 17, Application US/10095139  
; Patent No. US20020165357A1  
; GENERAL INFORMATION:





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Db      1 MEQEARVLRAGAGFGGARRL--IASAWVPCIVLGLVLSSEELLTAQAPAPCR-PDPPL 56
Qy      58 LSSAMR-----NNSVP-----LRLDGHEVHSCSRYLATIANPSAG 96
Db      57 LPPALALNKPALLDAITPLGFTTRASPCLLRYPD---PAPCTR----- 99
Qy      97 LEPGRVDLGLQLEBOESCLDGEFSOD--VYLSVTEWMLVCEENKVPDLTSLFVGV 154
Db      100 --PGPPAPARNGTCTGCTGMLYALPGAGLQSPVQMLVCGDGKVFLEQVSHLGL 157
Qy      155 LGSFVSGQLSDRGKRNVLFAIMAVQGSFLQISISWEMTVLFVIVMGQISNYVA 214
Db      158 LGCVIIAGGCDRGRRVAVASLVLTGTGASEALASFPDLLVLELHG-GTIAGALLA 216
Qy      215 FILG-TEILGKSVRIIFSTLGYCTEFVAVGMILLPLFAPIRDMRL-LALVYGVLCVP 272
Db      217 LYLARLECDPPHRLAFS-MGAGLFVSVGTLLPGIALVQDMRLQGLGALMSGILL- 274
Qy      273 LWMF---IDESPMLISORRFRREADIIOKAAMNNTAVPAVIFDSVEELNPKOOKA 329
Db      275 FMGFPLFPESPCLMATGQVARNARKILMRFAASVD-PG---DSPLEENSLATELTM 330
Qy      330 -----LDLFRF-----RNIAIMTMSILLMLTSVGYFALSIDAPMLGDAYLN 373
Db      331 SARSPQPRYHSPGLRTRVWNGLLGFSLSVGGIRASFRSLAPQVPTF---YLP 386
Qy      374 CFSALIEIPAYITAMLLRTLPRL-YIIAAVLFWGQVLLF---QLVP-VDIYFLSLG 428
Db      387 YFEAGLEAAALVFLITADCCGRPRVLLGTMVGLASLLLAGAQYLPVTVLFLV- 445
Qy      429 LVMLGFGITSASFMLVFTAEIPLTVLRNMAVGVTSTASVGSIIAPFYVIGAYNRML 488
Db      446 ---LGLASRAVASLSLFAAEVFPVIRGAGGIVLGAGFLGAQAPLDITLHGRGFTL 502
Qy      489 PIYMGSLVYLIGITFLFPESPGLMTLPETLEOMQVK 526
Db      503 QQVVFASLAVLALLCVLLPESSRSRGLPDSLADADRLR 540

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## RESULT 13

```

US-09-738-626-6795
; Sequence 6795, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, MAKOTO
; APPLICANT: SENO, AKIHITO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6795
; LENGTH: 448
; TYPE: PRN
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6795

```

```

Query Match      10.7%; Score 305.5; DB 9; Length 448;
Best Local Similarity 26.9%; Pred. No. 4.1e-18;
Matches 123; Conservative 62; Mismatches 190; Indels 83; Gaps 19;

Qy      116 GMEF-SQDV-----YLSVTEWMLVCEENKVPDLTSLF---FVGLLGSFVSGQLSD 165
Db      37 GVALDAMPVGLISFVMAALATWML-----SPTEMSLGSISFVGMALGASIGGLIAD 89
Qy      166 REGKRNVLFAFM---AVQGSFLQISISWEMTVLFVIVMGQISNYVAFLITGEIL 222
Db      90 KLGRQVRLSLIYGVATIGASAL---SVSLAMLMALFVGLGALPVASTLISFS 146
Qy      223 GKSVR-----IIFSTLGYCTEFVAVGMILLPLFAPIF---RDMRLIATLVPVLCVPL 273
Db      147 PRKVRGRNVILE-----AFNALGIMAIYGTFFVAGSDGWRMALALGCVPAIANYV 201
Qy      274 WMFIDESPMLISORRFRREADI---OKAAMNN---TAVPAVIFDSVEELNPKOOKA 327
Db      202 RLGLPESVRFLEKKGRHDEAELIVSFEEAAAEKADATVAVHDNAEGSVISMAA 261
Qy      328 FILDFFRRNTAIMINSLLMLTSVGYFALSIDAPL---HGDVINCFLSALI----- 380
Db      262 ---LRRRYALM-----IWFCTINLSYCAFTWIPSLVADGFTLVKSFQFTLLITLA 311
Qy      381 EIPAYITAMLLRTLPRIYIIAAVLFWGQVLLFVLQVVDYFLSIGVLMGFGITS 440
Db      312 QLPGYAVAAAMLLEKGRSTLATPLVGSALNGLANVMQILVAGCLL--SFPNIGA 369
Qy      441 FSMLYFTAEIPLTVLRNMAVGVTSTASVGSIIAPFYVIGAYNRMLPIYMGSLTVLI 500
Db      370 WQALYAIPELPLTVNRGTGAAAGFRISIIAPLV-----PPVIAFGPIALF 421
Qy      501 GFITLFPES--LGMTLPETLEOMQVKMFPSGKTRD 536
Db      422 ALFAFAIAIAIAFAFLPE-----OKGSLAD 448

```

## RESULT 14

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US-09-860-232A-7
; Sequence 7, Application US/09860232A
; Patent No. US2002028494A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: 57256 AND 58289, NOVEL HUMAN
; FILE REFERENCE: 381552001500
; CURRENT APPLICATION NUMBER: US/09/860, 232A
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205, 288
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 486
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-860-232A-7

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Query Match      9.8%; Score 280; DB 10; Length 486;
Best Local Similarity 26.1%; Pred. No. 7e-16;
Matches 119; Conservative 78; Mismatches 179; Indels 80; Gaps 15;

Qy      126 STVTEWMLVCEENKVPDLTSLFVGLLGSFVSGQLSDRFRGRN-----VLFATMAV 179
Db      48 STVLT-----GLVVSIFRIGRLISLFGKLGDRGRRKSLILALVFLVICAL 95
Qy      180 QRGFS--FLQFISISWEMTVLFVIVMGQISNYVAIITTEILGKSVR-----IIF 230
Db      96 LSGAAPGTTTIGLMAFVLLTVGRVAVLGAGVASVLYPMYISLAPKRLALGSLYOLA 155
Qy      231 STLGYCTEFVAVGMILLPL---FAVFI RDMRLIATLVPVLCVPLWMFIDESPMLISQ 287

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Db 156 ITGIIIVAAITGIGLNTKNDNSALNSWGRIPGLQVLPALLIGLILFESPRLVKEK 215  
QY 288 RRPREADIIQKAKAMNT-----AYPAVFEDSEVELNPKOOKATILDFRR---NTA 339  
Db 216 GKLEAEVEVAKLRGVEDVDQEOIEIKAELEAGVEE---EKAKASWGELEFRGTRPKVR 272  
QY 340 IMTMSLLMLTMSVGFALSLDAPNLH-----GDAYLNCFLSALLEIPAYITAMLLRT 394  
Db 273 QRLMGVMOLOFOQLTGINALFYFSPITFKSVGSDBASILVTIIGVAVNEFTVALIF 332  
QY 395 LPRRYITAAVLEWNG-----GVLLFIQVLPDYFSLISGLMKGFSITSA 440  
Db 333 LVDFRGRPRLILGAGMAICFLILGASIGVALLLNKPKDPLSKAGIYAVIFILLFIA 392  
QY 441 FSNL-----YVFTAEIYPTLVNMAVGVTASRVGSIIA---PYF-----VYLGAYN 485  
Db 393 FFALGCGPIPWILSELFPYKVRSKALALATANMLANFLIGFLFPYITGALGLAGY- 451  
QY 486 RMLPYIVGSLTVLIGIFTLF--PESIGMTLPETLE 520  
Db 452 ---VFLVFAGLVLVFLIFVFFVETKGRLEIEE 484

RESULT 15  
US-10-170-528-5  
; Sequence 5, Application US/10170528  
; Publication No. US20030009024A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: 46384, A Human Transporter Family Member  
; FILE REFERENCE: MPI01-092PIRM  
; CURRENT APPLICATION NUMBER: US/10/170,528  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: 60/298,012  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 488  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for PFAM PF00083  
US-10-170-528-5

Query Match 9.7%; Score 276.5; DB 9; Length 488;  
Best Local Similarity 25.2%; Pred. No. 1.4e-15;  
Matches 129; Conservative 83; Mismatches 186; Indels 113; Gaps 20;

QY 84 YRLATTANFSALGLEPGRDV---LGOLEOESCLDGEFSODPYLSTVTEWNLVCEDN 139  
Db 15 YDTGVIGGFLAL-----IDFLFRGLLTSSGAL-----AELVGYSTVLT----- 53  
QY 140 WKVPLTTSLEFVGVILGSFYSGOLSDRFGRKN-----VLFATMAVQTGS--FLQIFSI 191  
Db 54 ---GLVVSIFELRGLSLFAGKIDRFGRKKSLLTALVLFVIGALLSGAAPGYTTIGLM 110  
QY 192 SWEMFVLYFIYVGMQISNVVAFILGTTELIGKSVR-----LIESTIGVCTFFAVGYM 244  
Db 111 AFYLLLVGRVLVGLVGASVLPMTISELPKALRGALGSYQLAITTIGILVAAITIGLG 170  
QY 245 LRLP---FAFFINDMRMLLALTPGVLCVPLMWFIPESPRMLISORPREADIIQKAA 301  
Db 171 LKNTNDSALNSWGRIPGLQVLPALLIGLILFESPRLVKEKLEAEAREVL---A 227  
QY 302 KANNTAVPAVIFPSVELNPLKQ-----KATILDFR-----TRNIAIMTIA 344  
Db 228 KLGK-----VEDVDQEOIEIKAELEATVSEKAGASWGELEFRGTRPKVRQRLMGVY 281  
QY 345 SLLMLTSGVGFALSLDAPNLH---GDAYLNCFLSALLEIPAYITAMLLRTLPYRY 399

Db 282 LQAFOOLIGIN--AIFYSPITFKSVGSVASILVTIIVGVNFEVFTFALLIFLYDRF 339  
QY 400 IIAAVLFWNG-----GVLLFIQVLPDYFSLISGLMKGFSITSAFSL- 444  
Db 340 GRRPILLGAGMAICFLILGASIGVALLLNKPKDPSSKAGIYAVIFILLFIAFPALG 399  
QY 445 ---YVFTAEIYPTLVNMAVGVTASRVGSIIA---PYF-----VYLGAYNRMLPY 490  
Db 400 WGPPIWVILSELFPYKVRSKALALATANMLANFLIGFLFPYITGALGLAGY-----VF 455  
QY 491 IYVGSILVILIGIFTLF--PESIGMTLPETLE 520  
Db 456 LVFAGILVFLIFVFFVETKGRLEIEE 486

Search completed: July 3, 2003, 12:43:09  
Job time : 27 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2003, 12:35:54 ; Search time 51 Seconds

(without alignments)  
2818.424 Million cell updates/sec

Title: US-09-521-195B-1

Perfect score: 2845

Sequence: 1 MRDYDEVIAFLGEMGFQRL.....KTRDSMETEENPKVLTAF 551

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1203519 seqs, 260870444 residues 1203519

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCF\_NEW\_COMB.pep4:\*  
2: /cgn2\_6/ptodata/1/paa/PCF\_NEW\_COMB.pep4:\*  
3: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep4:\*  
4: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep4:\*  
5: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep4:\*  
6: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep4:\*  
7: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep4:\*  
8: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep4:\*  
9: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep4:\*  
10: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep4:\*  
11: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep4:\*  
12: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep4:\*  
13: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep4:\*  
14: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2845	100.0	551	US-10-327-189-7	Sequence 7, Appl
2	2839	99.8	551	US-10-327-189-38	Sequence 38, Appl
3	2833	99.6	551	US-10-327-189-2	Sequence 2, Appl
4	2218	78.0	557	US-09-949-016-6309	Sequence 6309, Ap
5	2218	78.0	557	US-10-327-189-4	Sequence 4, Appl
6	2166	76.1	551	US-60-453-135-12520	Sequence 12520, A
7	2166	76.1	551	US-60-453-135-12520	Sequence 12520, A
8	2166	76.1	551	US-60-453-135-12520	Sequence 12520, A
9	2166	76.1	551	US-60-453-135-12520	Sequence 12520, A
10	2034.5	50.8	564	US-09-949-016-7929	Sequence 7929, Ap
11	1445	50.8	304	US-10-326-820-2	Sequence 2, Appl
12	1445	50.8	304	US-09-724-676-96956	Sequence 96956, A
13	794.5	27.9	577	US-10-038-854-163	Sequence 96956, A
14	779.5	27.4	560	US-10-038-854-163	Sequence 163, App
15	740.5	25.0	534	US-10-038-854-38	Sequence 5604, App
16	714.5	26.1	526	US-10-038-854-30	Sequence 28, Appl
17	704	24.7	555	US-10-038-854-30	Sequence 30, Appl
18	704	24.7	555	US-60-453-135-13981	Sequence 105, App
19	704	24.7	555	US-60-453-135-13981	Sequence 13981, A

20	704	24.7	555	US-60-466-412-13981	Sequence 13981, A
21	703	24.7	555	PCT-US02-29560-248	Sequence 248, App
22	703	24.7	555	PCT-US02-19592-104	Sequence 104, App
23	703	24.7	555	US-10-243-882-248	Sequence 248, App
24	690.5	24.3	555	US-10-295-027-300	Sequence 300, App
25	685.5	24.1	554	US-10-038-854-371	Sequence 371, App
26	685.5	24.1	554	US-60-453-135-9175	Sequence 9175, App
27	685.5	24.1	554	US-60-453-135-9175	Sequence 9175, App
28	685.5	24.1	554	US-60-453-135-9175	Sequence 9175, App
29	673	23.7	535	US-10-219-051B-3126	Sequence 3126, App
30	673	23.7	535	US-10-219-051B-3130	Sequence 3130, App
31	673	23.7	535	US-10-219-051B-12729	Sequence 12729, A
32	673	23.7	535	US-10-219-051B-12733	Sequence 12733, A
33	671	23.6	556	US-09-949-016-7027	Sequence 7027, App
34	671	23.6	556	US-60-422-176-49	Sequence 49, Appl
35	671	23.6	556	US-60-453-135-13982	Sequence 13982, A
36	671	23.6	556	US-60-453-135-13982	Sequence 13982, A
37	671	23.6	556	US-60-466-412-13982	Sequence 13982, A
38	671	23.6	556	US-09-949-016-10036	Sequence 10036, A
39	654	23.0	547	US-09-949-016-7043	Sequence 7043, App
40	654	23.0	547	US-60-452-680-18592	Sequence 18592, A
41	653.5	23.0	456	US-10-038-854-164	Sequence 164, App
42	653.5	23.0	348	US-10-219-051B-3128	Sequence 3128, App
43	653.5	23.0	548	US-10-219-051B-3132	Sequence 3132, App
44	653.5	23.0	548	US-10-219-051B-12731	Sequence 12731, App
45	653.5	23.0	548	US-10-219-051B-12735	Sequence 12735, A

## ALIGNMENTS

```
RESULT 1
US-10-327-189-7
Sequence 7, Application US/10327189
GENERAL INFORMATION:
APPLICANT: Peltekova, Yanya D
APPLICANT: Rublin, Richard F
APPLICANT: Rublin, Laurence A
APPLICANT: Peter, St George-Hyslop H
APPLICANT: Simionovitch, Katherine A
TITLE OF INVENTION: POLYMORPHISMS OF THE OCTIN1 AND OCTIN2 CATION TRANSPORTERS ASSOC
FILE REFERENCE: ELLP-020
CURRENT APPLICATION NUMBER: US/10/327,189
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/362,700
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/343,338
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/427,529
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 60/362,717
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-10-327-189-7
Query Match 100.0%; Score 2845; DB 12; length 551;
Best Local Similarity 100.0%; Pred. No. 3.5e-250;
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRDYDEVIAFLGEMGFQRLIFFLSASITPNFGNGSVVFLAGTPEHRCRPDAANLSS 60
DB 1 MRDYDEVIAFLGEMGFQRLIFFLSASITPNFGNGSVVFLAGTPEHRCRPDAANLSS 60
QY 61 AMRNNVPLRLRGREVPSCSRRLATIANFSAIGLEPRVDVLDQLDQESCLDQWERS 120
DB 61 AMRNNVPLRLRGREVPSCSRRLATIANFSAIGLEPRVDVLDQLDQESCLDQWERS 120
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QY 121 QDYLSTVTETMNLVCEDNKKVPLTSLFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180  
DB 121 QDYLSTVTETMNLVCEDNKKVPLTSLFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180  
QY 181 TGFSFLOIFSIEMEFVLFVYVGMGOISNYVAFITGTEILGKSVRIIFSTLGVCTFEA 240  
DB 181 TGFSFLOIFSIEMEFVLFVYVGMGOISNYVAFITGTEILGKSVRIIFSTLGVCTFEA 240  
QY 241 VGYMLPLFAVFIKRMRLALATVPGLCVPLMWFIPESPRMLISORREAEEDIIOKA 300  
DB 241 VGYMLPLFAVFIKRMRLALATVPGLCVPLMWFIPESPRMLISORREAEEDIIOKA 300  
QY 301 AKANNVAPVAVIFDSVEELNPKQOKAFITLDFRTNIAIMTISLLMLTSGVYFALS 360  
DB 301 AKANNVAPVAVIFDSVEELNPKQOKAFITLDFRTNIAIMTISLLMLTSGVYFALS 360  
QY 361 LDAPNLHGDVYLNCFLSALIEIPAYITAMLLRTLPRTYITAAVLFMGGVLLFIQLVPY 420  
DB 361 LDAPNLHGDVYLNCFLSALIEIPAYITAMLLRTLPRTYITAAVLFMGGVLLFIQLVPY 420  
QY 421 DYYFLSIGVLMGKFGITSASFMLYFTAEPLTVRNMAVGVSTASRVGSIAPYFY 480  
DB 421 DYYFLSIGVLMGKFGITSASFMLYFTAEPLTVRNMAVGVSTASRVGSIAPYFY 480  
QY 481 LGAVNRMLPYIVMGSILVILGIFTLFPESLGMTLPETLEOMQKVMFRSGKRTDSMET 540  
DB 481 LGAVNRMLPYIVMGSILVILGIFTLFPESLGMTLPETLEOMQKVMFRSGKRTDSMET 540  
QY 541 EENPKVLITAF 551  
DB 541 EENPKVLITAF 551

## RESULT 2

US-10-327-189-38  
; Sequence 38, Application US/10327189  
; GENERAL INFORMATION:  
; APPLICANT: Peltekova, Yanya D  
; APPLICANT: Wintle, Richard F  
; APPLICANT: Rubin, Laurence A  
; APPLICANT: Peter, St George-Hyslop H  
; APPLICANT: Simnovitch, Katherine A  
; TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIAT  
; TITLE OF INVENTION: INFLAMMATORY BOWEL DISORDERS  
; FILE REFERENCE: ELP-020  
; CURRENT APPLICATION NUMBER: US/10/327,189  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: 60/362,700  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/343,338  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/427,529  
; PRIOR FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 60/362,717  
; PRIOR FILING DATE: 2002-03-08  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 551  
; TYPE: PR  
; ORGANISM: Homo sapiens  
US-10-327-189-38

Query Match 99.8%; Score 2839; DB 12; Length 551;  
Best Local Similarity 99.8%; Pred. No. 1.2e-249;  
Matches 550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MRDYEVIATLGEWGPFORLIFFLLSASITPENGFGMSVYVLAGTPEHRCVDPANLSS 60  
DB 1 MRDYEVIATLGEWGPFORLIFFLLSASITPENGFGMSVYVLAGTPEHRCVDPANLSS 60  
QY 61 AMRNNVPLRLRDGREVPHSCSRYLATIANFSALGLEPGRDVLGQLEQESCLDGEWS 120  
DB 61 AMRNNVPLRLRDGREVPHSCSRYLATIANFSALGLEPGRDVLGQLEQESCLDGEWS 120

DB 61 AMRNNVPLRLRDGREVPHSCSRYLATIANFSALGLEPGRDVLGQLEQESCLDGEWS 120  
QY 121 QDYLSTVTETMNLVCEDNKKVPLTSLFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180  
DB 121 QDYLSTVTETMNLVCEDNKKVPLTSLFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180  
QY 181 TGFSFLOIFSIEMEFVLFVYVGMGOISNYVAFITGTEILGKSVRIIFSTLGVCTFEA 240  
DB 181 TGFSFLOIFSIEMEFVLFVYVGMGOISNYVAFITGTEILGKSVRIIFSTLGVCTFEA 240  
QY 241 VGYMLPLFAVFIKRMRLALATVPGLCVPLMWFIPESPRMLISORREAEEDIIOKA 300  
DB 241 VGYMLPLFAVFIKRMRLALATVPGLCVPLMWFIPESPRMLISORREAEEDIIOKA 300  
QY 301 AKANNVAPVAVIFDSVEELNPKQOKAFITLDFRTNIAIMTISLLMLTSGVYFALS 360  
DB 301 AKANNVAPVAVIFDSVEELNPKQOKAFITLDFRTNIAIMTISLLMLTSGVYFALS 360  
QY 361 LDAPNLHGDVYLNCFLSALIEIPAYITAMLLRTLPRTYITAAVLFMGGVLLFIQLVPY 420  
DB 361 LDAPNLHGDVYLNCFLSALIEIPAYITAMLLRTLPRTYITAAVLFMGGVLLFIQLVPY 420  
QY 421 DYYFLSIGVLMGKFGITSASFMLYFTAEPLTVRNMAVGVSTASRVGSIAPYFY 480  
DB 421 DYYFLSIGVLMGKFGITSASFMLYFTAEPLTVRNMAVGVSTASRVGSIAPYFY 480  
QY 481 LGAVNRMLPYIVMGSILVILGIFTLFPESLGMTLPETLEOMQKVMFRSGKRTDSMET 540  
DB 481 LGAVNRMLPYIVMGSILVILGIFTLFPESLGMTLPETLEOMQKVMFRSGKRTDSMET 540  
QY 541 EENPKVLITAF 551  
DB 541 EENPKVLITAF 551

## RESULT 3

US-10-327-189-2  
; Sequence 2, Application US/10327189  
; GENERAL INFORMATION:  
; APPLICANT: Peltekova, Yanya D  
; APPLICANT: Wintle, Richard F  
; APPLICANT: Rubin, Laurence A  
; APPLICANT: Peter, St George-Hyslop H  
; APPLICANT: Simnovitch, Katherine A  
; TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOC  
; TITLE OF INVENTION: INFLAMMATORY BOWEL DISORDERS  
; FILE REFERENCE: ELP-020  
; CURRENT APPLICATION NUMBER: US/10/327,189  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: 60/362,700  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/343,338  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/427,529  
; PRIOR FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 60/362,717  
; PRIOR FILING DATE: 2002-03-08  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 551  
; TYPE: PR  
; ORGANISM: Homo sapiens  
US-10-327-189-2

Query Match 99.6%; Score 2833; DB 12; Length 551;  
Best Local Similarity 99.6%; Pred. No. 4.4e-249;  
Matches 549; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MRDYEVIATLGEWGPFORLIFFLLSASITPENGFGMSVYVLAGTPEHRCVDPANLSS 60  
DB 1 MRDYEVIATLGEWGPFORLIFFLLSASITPENGFGMSVYVLAGTPEHRCVDPANLSS 60

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RESULT 4
US-09-949-016-6309
; Sequence 6309, Application US/0949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6309
; LENGTH: 557
; TYPE: PRF
; ORGANISM: Human
US-09-949-016-6309

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Query Match	78.0%;	Score 2218;	DB 10;	length 557;
Best Local Similarity	75.9%;	Pred. No. 4.3e-193;		
Matches	423;	Conservative 57;	Mismatches 71;	Indels 6; Gaps 3
QY	1	MRDYEVIAPFGEMGFQRLIFELLASITIPGFMGMSVFLAGIPEHRCRYDPAANLSS	60	
Db	1	MDYDEVIAFGEMGFQRLIFELLASITIPGFMGMSVFLAIPERHRCRYDPAANLSS	60	
QY	61	AMRNNSVPLRLDGEVPPHSCSRYSRIATIANSSATGLEBGRVDYDGOLESCLDGMERS	120	
Db	61	AMRNITVPLRLDGEVPPHSCSRYSRIATIANSSATGLEBGRVDYDGOLESCLDGMERS	120	

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RESULT 5
US-10-327-189-4
; Sequence 4, Application US/10327189
; GENERAL INFORMATION:
; APPLICANT: Peltekova, Yanya D
; APPLICANT: Wintle, Richard F
; APPLICANT: Rubin, Laurence A
; APPLICANT: Peter, St.George-Hyslop H
; APPLICANT: Simnovitch, Katherine A
; TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSO
; FILE REFERENCE: ELP-020
; CURRENT APPLICATION NUMBER: US/10/327,189
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/362,700
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/343,338
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/427,529
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/362,717
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 557
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-327-189-4

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	Query Match	78.0%	Score 2218:	DB 12:	Length 557:
	Best Local Similarity	75.9%:	Pred No. 4, 3e-193:		
	Matches	Conservative	57:	Mismatches 71:	Indels 6:
					Gaps 3
QY	1	MRDYDEVIAFLGEMGFQRLIFPFLLSAIIIPNGFMGMVSVFLAGTPEHRCRVDPDAAI	SS	60	
			:		
Dd	1	MKDDEVIAFLGEMGFQRLIFPFLLSAIIIPNGFTGLSVPFLATPEHRCRVDPDAAI	SS	60	
			:		
QY	61	AARNSVPLKLDGGREVPHSCSRRIATATANSALGLEGRVDYLGOLFQESCDGWERS		120	

```
Db 61 AMRNHTVPLRLDRGKREVPHSCRRYRLATIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
QY 121 ODVYLSVTYEMNLVCEDMNKVPPLTSLFEVGVLLGSFVSGOLSDRGKRNVLFFATMAVQ 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ODVYLSVTYEMNLVCEDMNKAPLTLISLFEVGVLLGSFISGOLSDRGKRNVLFFATMAVQ 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 TGFSEFLOIFSISWEMFTVLVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEFA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 TGFSEFLOIFSISWEMFTVLVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEFA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 VGYMLPLFAFTRDMRMMLLATVPGVLCVPLMFTIPESPRMLISQRREREADIIQKA 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 VGYMLPLFAFTRDMRMMLLATVPGVLCVPLMFTIPESPRMLISQRREREADIIQKA 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AKANNTPAVPAVIFD--SVEELNPLKQOKAFILDLFRTNRNIAIMTMSILMLMTISVGYFA 358
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 AKANGIYVPSITFDPSLQDLSKQOOSHNIIDLRTNINRMVIMTMSILMLMTISVGYFG 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTPRRYIIAAVLFWGGVLLFTOLV 418
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 LSLDTPNLHGDIFVNCFLSAMVEVPAYVLAAMLLOYLPRRYSMATLFLGGSVLLFMQLY 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 419 PVDYFELSLGVMLGKRGISAFSMLYFPAELFPLVRMANGVSTASRGSIIAPYF 478
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 PDLTYLATVLMVGKFEVTAFAFSNVYTAELFPTVRNMGVSTASRGLSISPYF 480
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 479 VYLGAYNRMPLPYIVGSLVTLIGITLFEFPESLGMTLPETLEQOMQKWFPSRGK---KTR 535
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 VYLGAYDRFLPYILMGSLLITLALTFLPESFGTLPDPTIDOMLRYGKMKHRTTPSHR 540
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 536 DSMETEENPKVL-ITAF 551
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 MKDQGERPTILKSTAF 557
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
US-60-453-135-12520
; Sequence 12520, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12520
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-12520
```

```
Query Match 76.1%; Score 2166; DB 14; Length 551;
Best Local Similarity 74.9%; Pred. No. 2.3e-188;
Matches 417; Conservative 57; Mismatches 71; Indels 12; Gaps 4;
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```
QY 1 MRDYDEVIAFLGEMGPFQRLIFLLSASIIIPNGFNGMSVFLAGTPEHRCRVDPDANLSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRDYDEVIAFLGEMGPFQRLIFLLSASIIIPNGFNGMSVFLAGTPEHRCRVDPDANLSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AMRNNSVPLRLDRGKREVPHSCRRYRLATIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AMRNHTVPLRLDRGKREVPHSCRRYRLATIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 ODVYLSVTYEMNLVCEDMNKVPPLTSLFEVGVLLGSFVSGOLSDRGKRNVLFFATMAVQ 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ODVYLSVTYEMNLVCEDMNKAPLTLISLFEVGVLLGSFISGOLSDRGKRNVLFFATMAVQ 174
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 TGFSEFLOIFSISWEMFTVLVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEFA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 TGFSEFLOIFSISWEMFTVLVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEFA 234
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 241 VGYMLPLFAFTRDMRMMLLATVPGVLCVPLMFTIPESPRMLISQRREREADIIQKA 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 FGYMLPLFAFTRDMRMMLLATVPGVLCVPLMFTIPESPRMLISQRREREADIIQKA 294
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AKANNTPAVPAVIFD--SVEELNPLKQOKAFILDLFRTNRNIAIMTMSILMLMTISVGYFA 358
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 AKANGIYVPSITFDPSLQDLSKQOOSHNIIDLRTNINRMVIMTMSILMLMTISVGYFG 354
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTPRRYIIAAVLFWGGVLLFTOLV 418
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 355 LSLDTPNLHGDIFVNCFLSAMVEVPAYVLAAMLLOYLPRRYSMATLFLGGSVLLFMQLY 414
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 419 PVDYFELSLGVMLGKRGISAFSMLYFPAELFPLVRMANGVSTASRGSIIAPYF 478
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 415 PDLTYLATVLMVGKFEVTAFAFSNVYTAELFPTVRNMGVSTASRGLSISPYF 474
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 479 VYLGAYNRMPLPYIVGSLVTLIGITLFEFPESLGMTLPETLEQOMQKWFPSRGK---KTR 535
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 475 VYLGAYDRFLPYILMGSLLITLALTFLPESFGTLPDPTIDOMLRYGKMKHRTTPSHR 534
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 536 DSMETEENPKVL-ITAF 551
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 535 MKDQGERPTILKSTAF 551
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 7
US-60-453-050-12520
; Sequence 12520, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: LUKE, May
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12520
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-12520
```

```
Query Match 76.1%; Score 2166; DB 14; Length 551;
Best Local Similarity 74.9%; Pred. No. 2.3e-188;
Matches 417; Conservative 57; Mismatches 71; Indels 12; Gaps 4;
```

```
QY 1 MRDYDEVIAFLGEMGPFQRLIFLLSASIIIPNGFNGMSVFLAGTPEHRCRVDPDANLSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRDYDEVIAFLGEMGPFQRLIFLLSASIIIPNGFNGMSVFLAGTPEHRCRVDPDANLSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AMRNNSVPLRLDRGKREVPHSCRRYRLATIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AMRNHTVPLRLDRGKREVPHSCRRYRLATIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 ODVYLSVTYEMNLVCEDMNKVPPLTSLFEVGVLLGSFVSGOLSDRGKRNVLFFATMAVQ 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ODVYLSVTYEMNLVCEDMNKAPLTLISLFEVGVLLGSFISGOLSDRGKRNVLFFATMAVQ 174
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 TGFSEFLOIFSISWEMFTVLVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEFA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 TGFSEFLOIFSISWEMFTVLVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEFA 234
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 VGYMLPLFAFTRDMRMMLLATVPGVLCVPLMFTIPESPRMLISQRREREADIIQKA 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 FGYMLPLFAFTRDMRMMLLATVPGVLCVPLMFTIPESPRMLISQRREREADIIQKA 294
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AKANNTPAVPAVIFD--SVEELNPLKQOKAFILDLFRTNRNIAIMTMSILMLMTISVGYFA 358
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 AKANGIYVPSITFDPSLQDLSKQOOSHNIIDLRTNINRMVIMTMSILMLMTISVGYFG 354
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRLRYIAAVLFMGVGLFTOLV 418  
 Db 355 LSLDPTNLHGDIFVNCFLSAAVEVPAYLAWLLLOLYPRRSMAFLFLGSLVLLFMOLV 414  
 QY 419 PVDYFLSLGLVLMGKFGITSAFSLMYFAETALYPTLVLRNNAVGTSTASVGSIIAPYE 478  
 Db 415 PPDLYLATVLMVGMKFGVTAFAFSAVYVYTAELYPVVRNMGVSSVSTASRLGSIISPYE 474  
 QY 479 VYLGAYNMLPYIWMGSLTVLIGITLFFPESLGMTLPELLEOMQKVMKFRSGK---KTR 535  
 Db 475 VYLGAYDRFLPYILMGSLLITLITLTLFLPESFGTLPDITDMLRVKGMKRRTPSHTR 534  
 QY 536 DSMETEENKVL-ITAF 551  
 Db 535 MLKDGQERPTLKSTAF 551

RESULT 8  
 US-60-466-412-12520  
 ; Sequence 12520, Application US/60466412  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARCILL, Michele  
 ; APPLICANT: IAKOUTBOVA, Olga  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; FILE REFERENCE: CLO01466  
 ; CURRENT APPLICATION NUMBER: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
 ; CURRENT FILING DATE: 2003-04-30  
 ; NUMBER OF SEQ ID NOS: 429441  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12520  
 ; LENGTH: 551  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-466-412-12520

Query Match 76.1%; Score 2166; DB 14; Length 551;  
 Best Local Similarity 74.9%; Pred. No. 2.3e-188;  
 Matches 417; Conservative 57; Mismatches 71; Indels 12; Gaps 4;

QY 1 MRDVEYIAFLGEMGPFQRLIFPLLSAIIIPNGFGMSVVLGTPHRCVPAANLSS 60  
 Db 1 MRDVEYIAFLGEMGPFQRLIFPLLSAIIIPNGFGTGSVFLIATPEHRCVPAANLSS 60  
 QY 61 AMRNNSVPLRLRDGREVPHSCSRYLATIANFSALGLEPGRDVLQGLESCLDGWEFS 120  
 Db 61 AMRNHTVPLRLRDGREVPHSCRRRLATIANFSALGLEPGRDVLQGLESCLDGWEFS 120  
 QY 121 QDYYLSTVYTEMNLVCEDMNKVPLTSLFEVGVLLGSFVSGQLSDRFGKRVLEFATMAVQ 180  
 Db 121 QDYYLSTVY-----EDDMKAPLTLSLFEVGVLLGSFISGQLSDRFGKRVLEFATMAVQ 174  
 QY 181 TGFSLQIFSIWMEFTVLEVIYMGQISNYVAFLIGTELIGKSVRIIFSTLGVCTPFA 240  
 Db 175 TGFSLQIFSKNFEKFEVLEVIYMGQISNYVAFLIGTELIGKSVRIIFSTLGVCTPFA 234  
 QY 241 VGYMLPLFAFYIRDMRMLLALTPGVLCVPLMWFIPSPRWLISQRRFEAEADIIQKA 300  
 Db 235 FGYWVLPFAFYIRDMRMLLALTPGVLCVPLMWFIPSPRWLISQRRFEAEADIIIRKA 294  
 QY 301 AKMNTAVPAVIFD--SVEELNPLKQOKAFILDLFRTNIAIMTMSLLMLLTSVGYFA 358  
 Db 295 AKANGIYVPTIFDPSLELQDLSKKQOSHNLIDLRTWNIMRVIMSMIMMTISVGYFG 354  
 QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRLRYIAAVLFMGVGLFTOLV 418  
 Db 355 LSLDPTNLHGDIFVNCFLSAAVEVPAYLAWLLLOLYPRRSMAFLFLGSLVLLFMOLV 414  
 QY 419 PVDYFLSLGLVLMGKFGITSAFSLMYFAETALYPTLVLRNNAVGTSTASVGSIIAPYE 478  
 Db 415 PPDLYLATVLMVGMKFGVTAFAFSAVYVYTAELYPVVRNMGVSSVSTASRLGSIISPYE 474  
 QY 479 VYLGAYNMLPYIWMGSLTVLIGITLFFPESLGMTLPELLEOMQKVMKFRSGK---KTR 535

Db 475 VYLGAYDRFLPYILMGSLLITLITLFLPESFGTLPDITDMLRVKGMKRRTPSHTR 534  
 QY 536 DSMETEENKVL-ITAF 551  
 Db 535 MLKDGQERPTLKSTAF 551

RESULT 9  
 US-09-949-016-7929  
 ; Sequence 7929, Application US/09949016  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CLO01307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7929  
 ; LENGTH: 610  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-949-016-7929

Query Match 76.1%; Score 2166; DB 10; Length 610;  
 Best Local Similarity 74.9%; Pred. No. 2.6e-188;  
 Matches 417; Conservative 57; Mismatches 71; Indels 12; Gaps 4;

QY 1 MRDVEYIAFLGEMGPFQRLIFPLLSAIIIPNGFGMSVVLGTPHRCVPAANLSS 60  
 Db 60 MRDVEYIAFLGEMGPFQRLIFPLLSAIIIPNGFTGSVFLIATPEHRCVPAANLSS 119  
 QY 61 AMRNNSVPLRLRDGREVPHSCSRYLATIANFSALGLEPGRDVLQGLESCLDGWEFS 120  
 Db 120 AMRNHTVPLRLRDGREVPHSCRRRLATIANFSALGLEPGRDVLQGLESCLDGWEFS 179  
 QY 121 QDYYLSTVYTEMNLVCEDMNKVPLTSLFEVGVLLGSFVSGQLSDRFGKRVLEFATMAVQ 180  
 Db 180 QDYYLSTVY-----EDDMKAPLTLSLFEVGVLLGSFISGQLSDRFGKRVLEFATMAVQ 233  
 QY 181 TGFSLQIFSIWMEFTVLEVIYMGQISNYVAFLIGTELIGKSVRIIFSTLGVCTPFA 240  
 Db 234 TGFSLQIFSKNFEKFEVLEVIYMGQISNYVAFLIGTELIGKSVRIIFSTLGVCTPFA 293  
 QY 241 VGYMLPLFAFYIRDMRMLLALTPGVLCVPLMWFIPSPRWLISQRRFEAEADIIQKA 300  
 Db 294 FGYWVLPFAFYIRDMRMLLALTPGVLCVPLMWFIPSPRWLISQRRFEAEADIIIRKA 353  
 QY 301 AKMNTAVPAVIFD--SVEELNPLKQOKAFILDLFRTNIAIMTMSLLMLLTSVGYFA 358  
 Db 354 AKANGIYVPTIFDPSLELQDLSKKQOSHNLIDLRTWNIMRVIMSMIMMTISVGYFG 413  
 QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRLRYIAAVLFMGVGLFTOLV 418  
 Db 414 LSLDPTNLHGDIFVNCFLSAAVEVPAYLAWLLLOLYPRRSMAFLFLGSLVLLFMOLV 473  
 QY 419 PVDYFLSLGLVLMGKFGITSAFSLMYFAETALYPTLVLRNNAVGTSTASVGSIIAPYE 478  
 Db 474 PPDLYLATVLMVGMKFGVTAFAFSAVYVYTAELYPVVRNMGVSSVSTASRLGSIISPYE 533  
 QY 479 VYLGAYNMLPYIWMGSLTVLIGITLFFPESLGMTLPELLEOMQKVMKFRSGK---KTR 535  
 Db 534 VYLGAYDRFLPYILMGSLLITLITLFLPESFGTLPDITDMLRVKGMKRRTPSHTR 593  
 QY 536 DSMETEENKVL-ITAF 551

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Db      594 MKDQGERPTILKSTAR 610
: | | | |
RESULT 10
US-10-326-820-2
; Sequence 2, Application US/10326820
; GENERAL INFORMATION:
; APPLICANT: Thadd C. Reeder
; TITLE OF INVENTION: Organic Cation Transporter (OCTN3)
; TITLE OF INVENTION: Disruptions, Compositions and Methods Relating Thereto
; FILE REFERENCE: R-1493
; CURRENT APPLICATION NUMBER: US/10/326,820
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/342,490
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Targeting Vector
US-10-326-820-2

Query Match          71.5%; Score 2034.5; DB 12; Length 564;
Best Local Similarity 69.0%; Pred. No. 2.2e-176;
Matches 380; Conservative 75; Mismatches 85; Indels 11; Gaps 3;

QY      1 MRDYEVIAFLGEMGFQRLIFELLSASIIIPNGFNGMSVFLAGTPEHRCVDPDANLSS 60
      1 MLDYEVATLFGEMGFQRLIFELLSASIIIPNGFTGSAVFLAIEHRCRIPDVNLSS 60
Db      61 AMRNSVPLRLDGRVPHSCSRYLATIANFSALGLEPGRDVDLGQLEDSCLDGWEFS 120
      61 AMRNSHLPMTKGGPEVPQCRKRYRLATIANFSELGLEPGRDVLQLEDCNCLDGWEED 120
QY      121 ODVYLSVTVTENMLVCEENMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLPATMAVQ 180
      121 KQFLSTIVTEMVLCKDKDKAKPLTSLFVGVLLGSFISGQLSDRFGRKNILFLTMAMH 180
Db      121 KQFLSTIVTEMVLCKDKDKAKPLTSLFVGVLLGSFISGQLSDRFGRKNILFLTMAMH 180
QY      181 TGFSLQIFSIEMEFVLVYVGMQISNRYVAFILGTETILGKSVRIIFSTLGVCTFEFA 240
      181 TGFSLQIFSIEMEFVLVYVGMQISNRYVAFILGTETILGKSVRIIFSTLGVCTFEFA 240
Db      181 TGFSLQIFSIEMEFVLVYVGMQISNRYVAFILGTETILGKSVRIIFSTLGVCTFEFA 240
QY      241 VGYMLPLFAVFIKDMRMILLATLVPGVLCVPLMFIIPSPRMLISQGRKKEVEVITRKA 300
      241 FGFVPLPLFAVFIKDMRMILLATLVPGVLCVPLMFIIPSPRMLISQGRKKEVEVITRKA 300
Db      241 FGFVPLPLFAVFIKDMRMILLATLVPGVLCVPLMFIIPSPRMLISQGRKKEVEVITRKA 300
QY      301 AKMNMNTAVPAVIDSVSEELNPL-----KQKAFIIDLFTRTNIAIMTISLIMLMTSV 354
      301 AKINGIAPSTIFDP-SETKKLQDDSSKKPKQSHIYIDVTRPIRILTIMSIIMLMTISV 359
Db      301 AKINGIAPSTIFDP-SETKKLQDDSSKKPKQSHIYIDVTRPIRILTIMSIIMLMTISV 359
QY      355 GYFALSIDAPNLGDAYLNCFLSALIEIPAYITAMLLTLPRRYITAAVLEMGGVLLF 414
      360 GYGLSLDPLNGLNINYNCFLLAAVEPAAVYLAAMLLLOHVSRRYMAASLFLGSGVLLL 419
Db      415 IOVVPDYVPLSIGVLWLGKFTSAFSLMYVTAFLYVLAIVNNMAVGTSTASRGSITL 474
      420 VOLVPSDLATLSTLLVMWKGFTISAKMYVTAFLYVLAIVNNMAVGTSTASRGSITL 479
QY      475 APFYVYLGAAYNRMLPYIVMGSLTLVIGIFLFPESIGMTLPETLEOMQKRVWFRSGKKT 534
      480 SPFYVYLGAAYDRRLPITLMSGLTILFAITLFPESSGVSLPETIDEMQKVKKL-----KQ 535
Db      535 RDSMEIEENPK 545
      536 RQSLSKGSPK 546
```

RESULT 11  
US-09-724-676-96956

```
; Sequence 96956, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96956
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-96956

Query Match          50.8%; Score 1445; DB 10; Length 304;
Best Local Similarity 100.0%; Pred. No. 4.6e-123;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRDYEVIAFLGEMGFQRLIFELLSASIIIPNGFNGMSVFLAGTPEHRCVDPDANLSS 60
      1 MRDYEVIAFLGEMGFQRLIFELLSASIIIPNGFNGMSVFLAGTPEHRCVDPDANLSS 60
Db      1 MRDYEVIAFLGEMGFQRLIFELLSASIIIPNGFNGMSVFLAGTPEHRCVDPDANLSS 60
QY      61 AMRNSVPLRLDGRVPHSCSRYLATIANFSALGLEPGRDVDLGQLEDSCLDGWEFS 120
      61 AMRNSVPLRLDGRVPHSCSRYLATIANFSALGLEPGRDVDLGQLEDSCLDGWEFS 120
Db      61 AMRNSVPLRLDGRVPHSCSRYLATIANFSALGLEPGRDVDLGQLEDSCLDGWEFS 120
QY      121 ODVYLSVTVTENMLVCEENMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLPATMAVQ 180
      121 ODVYLSVTVTENMLVCEENMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLPATMAVQ 180
Db      121 ODVYLSVTVTENMLVCEENMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLPATMAVQ 180

RESULT 12
US-09-724-676A-96956
; Sequence 96956, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96956
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-96956
```

OY 181 TGFSFLOIFSIWMEFTVLFIYVGMQISNVVAFILGTETLGSVRIIFSTLGVCTFFA 240  
Db 181 TGFSFLOIFSIWMEFTVLFIYVGMQISNVVAFILGTETLGSVRIIFSTLGVCTFFA 240  
OY 241 VGYMLLPFAFIFIRDMRLILALTVPGVLCVPLMW 275  
Db 241 VGYMLLPFAFIFIRDMRLILALTVPGVLCVPLMW 275

## RESULT 13

US-10-038-854-163  
; Sequence 163, Application US/10038854  
; GENERAL INFORMATION:  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Li, Li  
; APPLICANT: Wolenc, Adam R  
; APPLICANT: Vernet, Corine  
; APPLICANT: Eisen, Andrew J  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Tcherev, Vellizar  
; APPLICANT: Spaderne, Steven K  
; APPLICANT: Gorman, Linda  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Paturajan, Meera  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Gangolli, Esha A  
; APPLICANT: Guo, Xiaojia S  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Caeman, Stacie J  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Gunther, Erik  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Macdougall, John R  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-230  
; CURRENT APPLICATION NUMBER: US/10/038,854  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: 60/258,928  
; PRIOR FILING DATE: 2000-12-29  
; PRIOR APPLICATION NUMBER: 60/259,415  
; PRIOR FILING DATE: 2001-01-02  
; PRIOR APPLICATION NUMBER: 60/259,785  
; PRIOR FILING DATE: 2001-01-04  
; PRIOR APPLICATION NUMBER: 60/269,814  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/279,832  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/279,833  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/279,863  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/283,889  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,447  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: 60/286,683  
; PRIOR FILING DATE: 2001-04-25  
; Remaining Prior Application data removed - See file wrapper or PAM.  
; NUMBER OF SEQ ID NOS: 411  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 163  
; LENGTH: 577  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-038-854-163

## Query Match

27.9%; Score 794.5; DB 12; Length 577;

Best Local Similarity 32.5%; Pred. No. 1,86-63; Matches 187; Conservative 117; Mismatches 222; Indels 49; Gaps 9;

OY 2 RDYDEVIATLGEWGPORLIFFLSASIIIPNGFNGSVYFLAGTEPHRCRV-----53  
Db 4 RHEGEGYDVHGHGRGRQRLYFICAFQNSCIIHLASVFMKVTTHHCRRPGNNSQYVF 63  
OY 54 -----DAANLSAMRNNSVPLRLRDGREVPS-CRRRLATIANFSAIGLEPGRDV 103  
Db 64 HNSNWSLDEDTGALLSCGQDYVTVOLONGEITMELSRCSRNKR---EWTSSIGYE-----115  
OY 104 DLGQLEOESCLDGMESODVYLTSTVTENINVCENMKVPLTSLFPGVLLGSVSGOL 163  
Db 116 YTGSKKEPPCVDGITYDONTMKTSTAYTQNLVCDKRWMLIQLPMEGVLLGSVYEGYF 175  
OY 164 SDFGRKRVLFATMAVOTGFSFLOIFSIWMEFTVLFIYVGMQISNVVAFILGTETLIG 223  
Db 176 SDRIGRRVYLMATSSMFLGIAAFVADYTFMARFPLANVAGVLYVGVYMEFIG 235  
OY 224 KSVRIIFSTLGVCTFFAVGYMLLPFAFIRDM---RMILLALTVPGVLCVPLMWIPES 280  
Db 236 MKSR-TWASVHLHSFPAVGTLLVLTGVLVRTMWLYOMILSTVTPFLICC---WVLPET 291  
OY 281 PMLISORPREAEDIIQKAKMNNTA-----VPAYIDSVSEELNPKQKAFILDLFR 334  
Db 292 PFWLSEGRYERAKYVDIMAKMNRASSCKSELSLDLOGVSVSPFEVQHNLSYLFY 351  
OY 335 TRNIAIMTMSLLMMLTSVGFALSLDAPNLHGDVYINCPLSALIEIPAYITAMLLRT 394  
Db 352 NMSIFKRTLVLMLIMFTGSLGYFSINSVNLGNMEYINLFLGVVEIPAYIFVCIADK 411  
OY 395 LPRRYIIANVLFWGGVLLFIQVLPYDYIFLSIGLVMGKFGITSFASMLYFAELTPT 454  
Db 412 VGRRTVLAISLFCALACGVAVVYIPQKHILGVVAVMKGFAIGAFIYLTYELTPT 471  
OY 455 LVNNMAVGTSTASRGSIITAPYFVLYGYNMLYIYVWGSITVYIGLFTFEPSLMT 514  
Db 472 IYRSIAVSGSNVCRASIIAPFVDSLSTWIFITQLVGVALLSGVLTLKLPETLGR 531  
OY 515 LPETLEOMQKVRWFRSGKRTDSMETENPKVLT 549  
Db 532 LATWEAAKL-----ESENESKSKILLT 556

## RESULT 14

US-10-218-140-5604

; Sequence 5604, Application US/10218140

; GENERAL INFORMATION:

; APPLICANT: Leach, Martin D.

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES

; FILE REFERENCE: 15966-543 CON

; CURRENT APPLICATION NUMBER: US/10/218,140

; PRIOR FILING DATE: 2002-08-12

; PRIOR APPLICATION NUMBER: 09/540,763

; PRIOR FILING DATE: 2000-03-30

; PRIOR APPLICATION NUMBER: 60/127,728

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: 60/127,636

; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: 60/127,607

; PRIOR FILING DATE: 1999-03-31

; NUMBER OF SEQ ID NOS: 6322

; SOFTWARE: Curator Version 1.0

; SEQ ID NO 5604

; LENGTH: 560

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-218-140-5604

Query Match

27.4%; Score 779.5; DB 12; Length 560;





Db 472 LLSGVLTKLPETLGRIATWEAAKL-----ESENESSKILLT 513

Search completed: July 3, 2003, 12:42:37  
Job time : 53 secs

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Db      541 TCGTCATGTCACCGAGTTTAACTGATGTGCCAATCCTCGATGTTGGACCTATTC 600
QY      582 ACCTCCCTGTTCTTCGAGCGGCTCCTCGCTCCTGCTCGGCGGACGCTGTCAGAC 641
Db      601 CAGTCATCACTGATGATGATGATTTATTTGGCTCATGATGATGATGATGATGATGAT 660
QY      642 AGGTTGGGAGGAAGAACGTTCTTCGCAACCATGCTGATAGACGCTGCTGCTGCTGCT 701
Db      661 AGGTTGGGCGGTAAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
QY      702 CTGCAAGATTTTCTCCATCAGCTGGGAGATGTTCTCTGTTATTTGTCATCGTGCGCATG 761
Db      721 CTGATGGCCATTTTCCCAACCTATACGTGATGTTATTTTGGCTTAATCAAGACAGCTG 780
QY      762 GGGCAGATCTCCCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 821
Db      781 GTACGAAAGCAGGCTGTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY      822 GTTCGATTAATTTCTCTATCATATGAGATGTCACATTTTTCGATGTTGCTATATGCTG 881
Db      841 TATCGGAGAACACTGGGGATTTTTCACAAATGGCTA---TACAGTTGGCTCCTGCTG 897
QY      882 CTGCGCACTGTTGCTTACTTCACTCAGACAGCTGGCGGAGTCTGCTGCTGCTGCTGCTG 941
Db      898 CTAGCTGGGGGTGCTTACGCACTTCTCTCACTGGAGGTGGTGCAGTTACAGTTGCTG 957
QY      942 CCGGAGATGCTGTGTCCCGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1001
Db      958 CCCAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1017
QY      1002 TCCGAGAGAAATTTAGAGAGGCTGAGATATATCCAAAAGCTGCAAAAATGAAACAC 1061
Db      1018 TCCCAAAAGAAATGCTGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATG 1077
QY      1062 ACAGCTGTATGAGCAATGATATTTGATTTGTGAGAGAGACTAAATCCCTGAGAGACAG 1121
Db      1078 AATATCTATCCGCTCCTCTTACGCGCTGAGACCTGTAAGAGAGAACTGGCAAAATG 1137
QY      1122 AAGCTTTATCTGTGAGCTGTTTCAGAGCTCGGAATATTCATATGATGATGATGATGAT 1181
Db      1138 AACCCTTATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
QY      1182 TTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1241
Db      1198 ATGTACACTGTTACAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1257
QY      1242 TTACATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
Db      1258 GCAGGTGACAAATATCTACTGATGATGATGATGATGATGATGATGATGATGATGATG 1317
QY      1302 ATTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1361
Db      1318 TTCAATGATCATCTATATGACCGCAATGCGAGCGTATACCTTTGGGCTGACATCAAT 1377
QY      1362 TTCTGGGGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421
Db      1378 ATGCTTGCAGGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437
QY      1422 TCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1481
Db      1438 AAAATTTATATCTATGCTTGGGAGAAATGAGGATCAAAATGAGGCTATGATGATGCT 1497
QY      1482 GTCTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
Db      1498 GTGGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1557
QY      1542 ACGGCTCTCAGAGTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1601
Db      1558 TCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1617
QY      1602 AGAAT---GCTGCTTACATGCTGATGATGATGATGATGATGATGATGATGATGATG 1658
Db      1618 TGGCTTGAAGCTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677

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QY      1659 CTTTTTCCCTGAAGTTTGGGATGATGATGATGATGATGATGATGATGATGATGATG 1718
Db      1678 CTGTTGCTCCAGAACTAAAGGAAAGCTTGGCTGAGACCTGAGAGAGCGGAAAT 1737
QY      1719 GTGAATGCTTCACTGCTGGGAAAAAA 1746
Db      1738 ATGCAAGACCAAGAAAAAATTAAGAA 1765

RESULT 2
US-09-040-444-6
; Sequence 6, Application US/09040444
; Patent No. 6063766
; GENERAL INFORMATION:
; APPLICANT: Koepsell, Hermann
; APPLICANT: Grundeman, Dirk
; APPLICANT: Gorboulev, Valentin
; TITLE OF INVENTION: Transport protein which effects the
; TITLE OF INVENTION: Transport of Cationic Xenobiotics and/or Pharmaceuticals,
; TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flanagan, Henderson, Farabow, Garrett & Dunner, L.L.P.
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,444
; FILING DATE: March 18, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: O'Connor, Steven P
; REGISTRATION NUMBER: 41,225
; TELEPHONE/DOCKET NUMBER: 2481.1453-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4400
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-040-444-6

Query Match      9.1%; Score 195.2; DB 3; Length 1896;
Best Local Similarity 48.5%; Pred. No. 3.6e-40;
Matches 596; Conservative 0; Mismatches 626; Indels 6; Gaps 2;

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QY	76	GGCCAGATCTCCAACTAATGAGTACGCTCATCTATGAGAAACGAAATTCCTGGCAAGCA	821
Db	781	GTACAGCAAGACGAGGTGGTTAATAGGCTACATCCTGATACGAATTTGTTGGGGGAGA	840
QY	822	GTTCGTATTAATATCTACATATAGAGATGTGACATTTTTCGACATGGCTATATAGCTG	881
Db	841	TATCGGAAACAGTGGGGATTTTTTACCAGATTGGCTA---TACATTTGGGCTCCGGTG	897
QY	882	CTGCCACTGTTGCTTACTTCAATCAGAGACTGGCGGATGCTGCTGTCGCTGACGGTG	941
Db	898	CTAGCTGGGGGTGGCTTACGCACTTCCTACCTGGAGGGGTGGTTCGACGTTCACTGTCGTG	957
QY	942	CCGGAGAGTGGTGTGTCGCCGTGGTGGTCAATTCCTGAATCTCCCGGATGGCGATTA	1001
Db	958	CCCAACTCTTCTTCTGCTCTATTACTGGTGCATACGTGACTGCTCCAGGTGGCTGATC	1017
QY	1002	TCCACAGAGAATTTAGAGGCTGAAGATATCATCCAAAAAGCTCCAAAAATGAAACAAC	1061
Db	1018	TCCAGAAATTAAGAAATGCTGAAGGCATGAGATCATTTAAGCAATCGCAAAAGAAAATGA	1077
QY	1062	ACAGCTGTACAGACAGTATATTTGATTTCTGTGGAGAGCTAAATCCCTGAACACAG	1122
Db	1078	AAATCTCTACCCGCTCCCTTCACAGCGCTGAGACTTGAAAGAGAAATGGAAGAAATYG	1137
QY	1122	AAAGCTTCATTTCTGAGACCTGTGACAGCTGCGAATATTCACATTAATGATCT	1181
Db	1138	AAACCTTCACTTTCTTGACTTGGTGTAGAACTCTCAGATTAAGAAACATATCATGATATGG	1197
QY	1182	TTCCTGTATGATGCTGACCTCAGTGGGGTATCTTTCCTGCTGCTGTGATGCTCTAAT	1241
Db	1198	ATGTACAATGGTTTACAGAGCTCTGTGCTACCAAGGGCTCATATGACATAGAGGCTTT	1257
QY	1242	TTACATGAGAGATGCTACCTGACTGTTTCTCTCTGCTTATTTGAATTCAGGTTAC	1301
Db	1258	GGAGGTGACAAATATCTACCTGGAATTTCTTCTACCTGCCCCGTGGTGAATTCGACGTGTC	1311
QY	1302	ATTACAGCCTGGCTCTATTTGCGAAGCGTGCCAGGGGTATATTCATAGCTGACGATACG	1361
Db	1318	TTTCAATGATATTCCTATTAATGACGCCGATGGGAGCGGTTACCTTGGGCTGATCAAT	1377
QY	1362	TTCTGGGGAGAGGTGTGCTTCTCTTCAATTCACATGATGATCTGTGATTAATTAATCTTTA	1421
Db	1378	ATGATGTGACGGGGAGCGCTGCTGGCCCTCAGTTTATTAATCTGGTATCTACAATGGCTA	1437
QY	1422	TCCATTTGGTCTGCTATGCTGGGAAATTTTGGATTCACCTCTGCTTTCTCCATGCTGAT	1481
Db	1438	AAATATTAATATCTCATGCTTGGGAAAGATGGGGATCAATGGCGTATGAGATAGCTCTGC	1497
QY	1482	GTCCTACATGCTGACCTTACCCAAACCTGTGTGAGGAACATGGGGGGGGGCTGACATCC	1541
Db	1498	CTGTGCTAATGCTGACCTGTACCCCACTTCAATTAGGAATCTTGGCGTCCACATCTGTCC	1557
QY	1542	ACGGCCTCCAGAGTGGGAGACATATGCCCCCTACATTTGTTTAACCTCGGTGCTTAAC	1601
Db	1558	TCAATGTGTGACATTTGTGGCATCATACGCCATTTCCGTGCHACACGGCTCATTAATTC	1617
QY	1602	AGCAAT---GCTGCCCTAATGCTCATGGGTAGTGTGACTGTCTCGATTTGGAATCTTCACC	1651
Db	1618	TGGCTTGACCTCCCGCTATAGTTTTCGGCGTACTTGGCTTGGTGTGCTGAGAGTCTGTGG	1677
QY	1659	CTTTTTCCTCCGAAAGTTTGGGAATGATCTTCCAAAAACCTTAAGACATGACGAGAA	1711
Db	1678	CTGTCTCTCCGAAACATTAAGGGAAACCTTTGCTGTAGACATCGAGAGAGCGGAAAT	1737
QY	1719	GTGAAATGCTCAGATCTGGGAAAAAA 1746	
Db	1738	ATGCAAAAGACCAAGAAAAATTAAGAAA 1765	

```

Patent No. 6063623
GENERAL INFORMATION:
APPLICANT: Koepsell, Hermann
APPLICANT: Grundenman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport of protein which effects the
TITLE OF INVENTION: Transport of cationic xenobiotics and/or pharmaceuticals
TITLE OF INVENTION: DNA sequences encoding it and their use.
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,572
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Toohey, Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1453-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1882 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-501-572-4

Query Match      8.2%; Score 175; DB 3; Length 1882;
Best Local Similarity 47.5%; Pred. No. 5,1e-35;
Matches 585; Conservative 0; Mismatches 640; Indels 6; Gaps 2;

QY      522  TCCACCGCTGATGACCGAGTGGAAATCTGCTGTGTGAGACACTGGAAAGTCCCTCACC 581
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      434  TCTCATCGTCACCTGAGTTTAACTGCTGTGTGAGAACGCCCTGGAAGTGAGACTTTT 493
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY      582  ACCTCCTGTTCTTCGTAGAGCGTCTCTCGGCTCTTCGTGTCCGGGACGCTCTCAGAC 641
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      494  CAGTCTGTGTGAACCTTGGGCTTTCTTCTGTGGCTCCCTGGTGTGGGGTAACTTGCAGAC 553
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY      642  AGCTTTGGCAGAGAAAGAGTCTCTCTTCCGCAACATGGCTGTACAGACTGGCTTCAGCTTC 701
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      554  AGTTTGGCCGTAAAGCTCTGTCTTCTTGTGTGACACAGCGTGTGCACATGTGTCCGGTGTG 613
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY      702  CTGCAGATTTTCTCCATCAGCTGGGAGATGTTCACTGTGTATTGTTCATGTGTGGCATG 761
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      614  CTAACAGCGGTGGCCGCCAGACTATACATCCATGTTGCTCTTCCCTGCTGTCAGAGGATG 673
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY      762  GGCCAGATCTCCACACTATGTGGTACGCTTCACTACTAGGACAGAAATCTTGCAAGTCA 821
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      674  GTCAAGCAAGGCGACGTGGGTGTCCGGGTATACCTGTGATCAACAGAGTTGTGTGGC---TCT 730
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY      822  GTTCGATTATATTCTCTACATTAAGAGAGTGACACATTTTTCGACATGTTGGCTATATGCTG 881
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      731  GGCTACAGGAGAAAGACAGCGCCATTTTGTACCAAGATGGCTTCCACAGTGGGCTATGGGG 790
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY      882  CTGCACACTGTTTGTCTTACTCATGAGAGACTGGGGAGATGCTGTGCTGGCCCTAGACGGTG 941
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      791  CTGTCCGGGGGTGGCCCTATGCTCATTCACAGACTGGCGCTGCTCCAGCTATGCTGTCTCCTG 850
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

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QY	942	CCGGAGAGCTGCTGTCGCGCGCTGGGAGTTCATTCCTGAAATCTCCCGATGGCTGATA	1001
Db	851	CCCTACCTTCCTTCCTCTCTCTATTTACTGTTTGCCGAGATCCCCCGGTGGCTGTG	910
QY	1002	TCCGAGAGAAGATTTAGAGAGCTGAAAGTATTCATCCAAAAGCTGCAAAAATGAAAC	1061
Db	911	TCCCGAGAGAACACCGACGCTGTGAGATTAATGAGCAAAATTCGACAGAAAGAGGG	970
QY	1062	ACAGCTGTACACGACATGATATTTGATTTCTGTGGAGAGCTAAATTCCTGAGCAGAC	1121
Db	971	AAGGTCCTCTGCTGACCTGAAAGTCTGTGCTTTAAGAGAGATGCTGCAAAAACGA	1030
QY	1122	AAAGCTTTCATTTCTGAGACCTGTTCCAGACCTGGAAATATTCGCAATATGACCATATGCT	1181
Db	1031	AGTCCTTGTTGGCGAGACTGTTCGCGACTCCCACTGAGAGAGCACCCTGATCTCTG	1090
QY	1182	TTGCTGCTATGGAATGCTGACCTCACTGAGGTTACTTTGCTGTCTGTGATGCTCTAAT	1241
Db	1091	ATGATATCATGTTGTTCTCTGTGCTGTGCTGATGAGGCTTCATCATGACACATGGAGACC	1150
QY	1242	TTACATGAGATGAGCTACCTGACCTGATGTTTCTCTGCTGCTGATTAATTCAGCTTAC	1301
Db	1151	ACAGGGGCGAACCTCTACCTGATGATTTCTTTATTTCTCTCTGAGGAAATTCGCCGCGCC	1210
QY	1302	ATTACAGCTTGCTGCTATTTGCGAACCTGCGCCAGGCGTTATATCATAGCTGCAACTG	1361
Db	1211	TTTCATCATCTCTGCTACCATTTGACCGGATTTGGCCGACATCAACCAATAGCGCTGAAAT	1270
QY	1362	TTCTGGGAGAGAGGTGCTGCTCTCTTCATTTCACTGAGTACTGTGATTTATCTTCTTA	1421
Db	1271	CTGCTGACAGGGGGGACGCTGCTCTCTATGATCTTTATCCCGCATGAGCTGCTGTTG	1330
QY	1422	TCCATTTGCTGTGTCATGCTGCGGAAAAATTTGGATCACCTCTGCTTCTCCATGCTGTAT	1481
Db	1331	AACCTTACCCCTCGCCTGTCTTGGCGGATGAGGGGCCACCAATTGCTGTCAGATGTCGTGC	1390
QY	1482	GTTCTCATCTGTGAGCTCTACCCCAACCTGTGTGAGAGAACATGCGCGTGGGGGTGCATCC	1541
Db	1391	CTGCTGACAGCTGTGAGCTGTACCTCTACATTTATCATGGAATCTTGGAGATGAGATTCCTCT	1450
QY	1542	ACGGCCTTCAGAGTGGGACAGCATATGCCCCCTACTACTTTGTTTAC--CTCGATGCTTAC	1598
Db	1451	GCCCTGTGTGACCTGGGTGGGATCTTCAACCCCTCTCATGTTGTTGACGCTGATGAAAGTT	1510
QY	1599	AACGAAATGCTGCCCCCTACATCTGATGGAATGCTGACTCTCTGATTTGGAATCTTCAAC	1658
Db	1511	TGCGAACCCCTCGCCCCCTATTTGTTTGGGATTTTGGCCCTGACTGTGGGGCCATGACT	1570
QY	1659	CTTTTTCCTCTGAAATTTTGGGATGATCTTTCAGAACTTTAGAGCAGATGATGAGAA	1718
Db	1571	CTTCTTCTCCAGAGACCAAGGGTGTGCTTTGCTGTGAGACTTTGAAGAAGCAGAGAAC	1630
QY	1719	GTGAATGTCTCAGATCTGGGAAAAAACAA	1749
Db	1631	CTGGGAGAGGAGGAATCAAGGCCAAAGAAA	1661

RESULT 4  
 US-09-040-444-4  
 Sequence 4, Application US/09040444  
 Patent No. 6063766  
 GENERAL INFORMATION:  
 APPLICANT: Koepsell, Hermann  
 APPLICANT: Grundeman, Dirk  
 APPLICANT: Gorboulev, Valentin  
 TITLE OF INVENTION: Transport protein Which Effects The  
 TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals,  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan,Henderson,Farabow,Garrett & Dunner, L.L.P.  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington

```

1  STATE: D.C.
2  COUNTRY: USA
3  ZIP: 20005-3315
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE: Floppy disk
6  COMPUTER: IBM PC compatible
7  OPERATING SYSTEM: PC-DOS/MS-DOS
8  SOFTWARE: Patent.in Release #1.0, Version #1.30
9  CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/09/040,444
11 FILING DATE: March 18, 1998
12 CLASSIFICATION:
13 ATTORNEY/AGENT INFORMATION:
14 NAME: O'Connor, Steven P
15 REGISTRATION NUMBER: 41,225
16 REFERENCE/DOCKET NUMBER: 2481.1453-01
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (202)408-4000
19 TELEFAX: (202)408-4400
20 INFORMATION FOR SEQ ID NO: 4:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 1883 base pairs
23 TYPE: nucleic acid
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26 MOLECULE TYPE: DNA (genomic)
27 US-09-040-444-4

```

Query Match	8.28;	Score 175;	DB 3;	Length 1882;
Best Local Similarity	47.58;	Pred. No. 5.1e-35;		
Matches 585; Conservative	0;	Mismatches 640;	Indels 6;	Gaps 2

QY	522	TCACAGCTGCTAACCGAGGAGAAATCTGGGTGTGTGAGAACAACTGGAAAGGTGCCCTCAC	581
Db	434	TCCTCCATGCTACAGTGGATTAACTGGGTGTGTGAGAACGCTGGAAAGTGGACCTTTT	493
QY	582	ACCTCCCTGTTCTCTGTGAGGCGTGTCTCTGGGCTCTTGTCGTGTCGGGCGAGCTGTACAG	641
Db	494	CAGTCTCTGTGTAACTTGGGCTTCTTCCGTGGGCTCCCTGGTGTGGGTATCATTTACAGAC	553
QY	642	AGGTTGGCAGGAACAGAGTCTCTTCGCACACATGGGCTGTACACATGCGCTTCAGCTTC	701
Db	554	AGGTTGGCCGTAACTCTGTCTCTTGGAGACACGCTGTGTACATCTGTGTGCCGGTGTG	613
QY	702	CTGCAGATTTTCTCCATCAGCTGGGAGATGTTCACCTGTGTATTTGTATCGTGGGCAATG	761
Db	614	CTAACAGCGGTGGCCCCAGACTATACATCACTAGTTGTCTTTGGCTGCTGTGAGGGCANTG	673
QY	762	GGCCAGATCTCCAACTATGTGGTAGCCTTCACTAGAGACAGAAATCTTGGCAGATCA	821
Db	674	GTCAAGAGGGGAGGTGGGTGTCCGGCTATACCTTGATATCAGAGATTTGTGTGGC---	730
QY	822	GTTCTATTATATTTCTATACATTTAGAGATGTGCACATTTTTCGAGTTGGGCTATATGCTG	881
Db	731	GGCTACAGGAGAACACAGGCCCATTTTGTATCCAGATGGCCTTACACAGTGGGCTAGTGGGG	790
QY	882	CTGCCACTGTTTGTCTTACTTATCATCAGAGACTGGCGGATGCTGTCTGGCCTGCAGGGTGTG	941
Db	791	CTTGGCGGGGTGGCCTATGATCCATTCACAGCTGGGCGCTGGCTCCACCTAGCTGTGTGCCGTG	850
QY	942	CCGGGAGTGTGTGTGTCCCGCTGTGGTGTTCATTTCTGAAATCTCCCGATGGCTGATA	1001
Db	851	CTTACTCTCTCTTCCCTGTGCTGTATTTACTGGTTTGTCCAGAAATCCCCCGGTGGCTGTGTG	910
QY	1002	TCCAGAGAAATTTAGAGAGCGGTGAATATPACATPCCAAAAGCTGCCAAAATATGAACAA	1061
Db	911	TCCAGAGAAACACCGGAGCTGTCTAGATTAATGGCAAAATTTGCACAGAAAGACGGG	970
QY	1062	ACAGCTGACAGCAGAGTGAATTTGATTTCTGTGAGAGAGCTAAATPCCCTGAACAGCAG	1121
Db	971	AAAGTGCCCTCTGTGTGACCTGAAGATGTCTGTGCTTGAAGAGAGTGCCTCAGAAAAGGA	1030
QY	1122	AAAGCTTTCATTTGTGAGACTGTGTAGAGCTTCGGAATATTTGCCATTAATGACATTATGTCT	1181

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1031 AGNCTTGTGTTGGCCGACCTGTTTCCGACCTCCCAACCTGAGGAAACACACCGCTATCTCGT 1090
QY 1182 TTGCTCTGTATGGATGCTGACCTCAGTGAGGTTACTTTGCTCTGTCTCTGGATGCTCTTAAT 1241
Db 1091 ATGTATCTATGTTGTTCTTGTGTGCTGTGCTACCAAGGGCTCATCATGACGACCTGGAGGC 1150
QY 1242 TTTCATGAGGAGATCCCATACCTGAAACGTTTTCCTGCTGCGCTGATTTGAAATTCACAGCTTAC 1301
Db 1151 ACAGGGGCCAACCTCTACCTGACACTCTTTTATCTTCTCTGTGTGAATTTCCCGCGGCC 1210
QY 1302 ATTACAGCCTGCGCTGTATTGCGAAGCGTGGCCAGGCGTTTATATCATAGCTGACAGTACTG 1361
Db 1211 TTTCATCATCTGTGTATCCATATGACCGCATTTGGCCGCGCATCTACCAATACCGGCGCTGAAAT 1270
QY 1362 TTCTGGGGAGAGAGTGTGCTCTCTCTCATTTCAACTGTGACGTGCGTGAATATTAATTCTTTA 1421
Db 1271 CTGTGTACGGGGGACAGCTGTGCTCTCTCATGATCTTTATCCCGCATGAGCTGCACGTGTGG 1330
QY 1422 TTCCATGTGTTGTGTTCAATGCTGGGAAATTTGGAGATACCTCTGCTTTCTCCATGCTGTAT 1481
Db 1331 AAGTTTACCTCGCCCTGCTGTCTGGCCGTATAGGGGGCCACCATGTGTGTGAGATGGTGTGCTG 1390
QY 1482 GTCTTCACTGTCTAGCTCTTACCAACCTGTGTGAGGAAACATGAGCGGTGGGGGTCAATCC 1541
Db 1391 CTGTGTGAACCTCTAGGTGTGATACCTCATTTATCATGAGAAATCTGGGATGATGATTTGCTCT 1450
QY 1542 ACGGCGCCGAGTGTGGGCAAGCATCATTTGGCCCCCTTATTTTGTTTAC--CTCGTGTGCTTAC 1598
Db 1451 GCCCTGTGTACCTGTGGGTGGGATCTTCACACCCTTATGTGTGTACAGGCTGATGGAAGTT 1510
QY 1599 AACAGATGCTGTGCCCTCATATGTCATAGGTGTGATGTGATGCTGATGCTGATTTGAAATCTTAC 1658
Db 1511 TGCGAAGCCCTGTGCCCTCATTTTGTGTTGGGGTTTGTGGGCTGACTGTGGGCCATGACT 1570
QY 1659 CTTTTTTTCCCTGAAGTTTGGGAATGACCTCTCCAGAAACCTTAAGAGATATGCGAATA 1718
Db 1571 CTCTCTCTCCCAAGACCAAGGCTGTGGCTTGTGCTGTGAGACTATTTGAAGAAGCAGAGAAC 1630
QY 1719 GTGAATATGTTTCAGATCTGTGGAAAAAACA 1749
Db 1631 CTGGGAGGAGGAAATCAAAAGGCCAAGAAA 1661

RESULT 5
US-08-501-572-5
: Sequence 5, Application US/08501572
: Patent No. 6063623
: GENERAL INFORMATION:
: APPLICANT: Koepsell, Hermann
: APPLICANT: Grudeman, Dirk
: APPLICANT: Gorboulev, Valentin
: TITLE OF INVENTION: Transport protein which effects the
: TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
: STREET: 1300 I Street, N.W., Suite 700
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/501.572
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Toohey, Kimberlin M
; REGISTRATION NUMBER: 35,391
; REFERENCE/DOCKET NUMBER: 02481.1453-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1885 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-501-572-5

```

	Query Match	8.2%	Score 174.8	DB 3	Length 1885	
	Best Local Similarity	48.4%	Pred. No. 5.8e-35			
	Matches 612	Conservative 0	Mismatches 637	Indels 15	Gaps 4	
QY	457	ACCTGGGGCAGCTTGAGCAGAGAGAGCTGCCGTGATGCGTGGAGGTTACGCCAGAGCTCT	516			
Db	407	ACAGAGGACCACTCCCGCTGGGTCCTCCGCCAGATGGCTGGGGTWT-----ATGACAGCG	460			
QY	517	ACCTGTCCAGCTGTGTACCGAGTGGAAATCGATGTGTGGAGACACATGGAAAGTGGCCCC	576			
Db	461	CCGGCTCTTCATGTCTACGTAGTTCACACCTGGGTGTGTCTGCTACTCTGGAACTGGACC	520			
QY	577	TCACCACCTCCCTCTTCTCTGTAAGCGGTGCTCCGCGCTCTGCTGTGTCCGGGACGTGT	636			
Db	521	TCTTTCACTCCTGTTTGAATGACGGGCTCTCTTGTGGCTCTCTCGGTGTGGTACTTTG	580			
QY	637	CAGACAGGTTTGGCAGAGAAAGACGTCTCTTCGACACCAATGGCTGTACAGACTGGCTCA	696			
Db	581	CAGAGAGTTTGGCCGTGAAGCTGTGTCTCCCTGGAGAACTGTGTCTCAACCGGTTGGG	640			
QY	697	GCTTCCTCCATATTTTCCCATCCAGCTGGAGATGTTCACGTGTATTGTTCATCTGAG	756			
Db	641	GCGTCTCATG6GCGTCTCGGCCAATCATATGTCATGCTGCTCTCTCGCGCTGCAGG	700			
QY	757	GCATGGGCGAATCTCCAACTATGTGTGTAGCTTTCATCTAGAGAACAAATTCCTGGCA	816			
Db	701	GCGTGTGTAGCAAGGGCAACTGGAATGGGTGGCTACACCTTAATCAACAATTTGTGGCT	760			
QY	817	AGTCAGTCTGATTTATCTCTACTATAGAGAGTGTGCACATTTTTCAGTTGGCTCTA	876			
Db	761	CGGGCTCCAGAAAGACGCTGGGGATCATGTACAG--ATGGCCTTACGGGGGGGCTGG	817			
QY	877	TGCTCTGCCACTGTTTGTCTACTTCTATCAGACAGACTGGCGGATGTGCTGTGGGCTGA	936			
Db	818	TGGCCTCTTACCGGGCTGGCTACGCCCTGCTCATGTGGCGGTGAGGTGGTGAAGTCT	877			
QY	937	CGGTCCCGGAGTGTGTGTGTGCCCGCTGGGTGGTTCATTCCTAATCTCCCGATGCG	996			
Db	878	CCCTCCACCACTCTCTCTCTCTGCTCTACTACTGTGTGTGTGGGGAAGTCCCTCGTGGG	937			
QY	997	TGATATCCACAGAAATTTAGAGAGCTGAAGATATATCCAAAAAGCTGCMAAAATGA	1055			
Db	938	TGTTATTCACAAAAAGAAACACTGACAGCAATTAATATATGACACATCGCTCAAAAAG	997			
QY	1057	ACAACACAGCTGTACACAGAGATGATTTTGTATTTGTGGAGAGCTAATCCCTCGAAGC	1116			
Db	998	ATGGGAATGTGCTCTCTGCTGATTTAAAGATCTTTCCCTCGAABAAGAGATGTACACGAA	105			
QY	1117	AGCAGAAAGCTTTTCATTTCTGACCTGTTCAGAGCTCGGAAATATTCCTATATGACCATTA	1177			
Db	1058	ACCTAGAGCCTTCATTTTGGAGACTGTGTCCGACCCCGCCCTGAGAGAGCGCACCTTCA	1117			
QY	1177	TGCTGTGTGTATGATGAGTGCAGCTAGTGAAGGTACTTCTCTGTCTGTGATGTGCTC	1236			
Db	1118	TCTGTATGTACTGT	1177			
QY	1237	CTAATTTACATGAGAGATGCTACCTGAACCTGTTCTCTCTGCTTGTATGAAATTCAG	1296			

Db 1178 GCGGCACAGGGGGAGACCTCTACCTGGATTTCCTTAATCTCCGTCTGTGGAAATCCCG 1237

QY 1237 CTTCATTACAGCCTGGCTGCTATTGGCAACGCTGCCAAGCGTTATATCATAGCTGCAG 1356

Db 1238 GGGCCCTCATGAGCCCTCATCACCATTTGACCGCGGGCCGCATCTACCCATGGCGGT 1297

QY 1357 TACTGTTCTGGGAGAGAGTGCTGCTCTCTCATTTCACTGATCGTACCGTGGATTATTA 1416

Db 1298 CAATTTGTTGGCGGGGGACGCCCTGCTGTCATTTTATCTACCT--GACCTGCAC 1354

QY 1417 TCTTATTCATTGGTCTGGTCAATGCTGGGAAATTTGGGATCACCTGCTTTCTCCATGC 1476

Db 1355 GGTAAACATCATATATATATGTGTGTGGCCGAATGGGAATACCATTTCAATACAAATGA 1414

QY 1477 TGTATGCTTCACTGAGTGCTGATACCCAAACCCGTCGACAGAAATAGGCGGTG 1336

Db 1415 TCTCCGCTGGTAATGCTGAGCTGTACCCCAATTCGACAGAACTTAGATTAAGTGT 1474

QY 1537 CATCCAGGCGCTCCAGAGTGGGAGCATCATTTGCCCTCATTTGTTTAC--CTCGGTG 1593

Db 1475 GTTCTCCCTGCTGTGACATAGTGGAGTAATACACCCCTCATATAGTTCAGGCTGAGGG 1534

QY 1594 CTTCACACAGAAATCTGCTCCCTACATCTCATAGGTAGTGCAGCTGCTCATTTGGAATCT 1653

Db 1535 AGCTCTGGCAAGCCTTGCCCTCATTTTGTGTGGGTGTGGGCGCTTGCCGCGGAG 1594

QY 1654 TCACCCCTTTTTCCTGAAAGTTTGGGAATGACTCTTTCAGAAACCTTAGACAGATGC 1713

Db 1595 TGACGCTACTTCTTCCAGAGACCAAGGGGAGCGTTTGCCAGAGACCATTAAGAGACGCC 1654

QY 1714 AGAA 1717

Db 1655 AGAA 1658

RESULT 6  
US-09-040-444-5  
Sequence 5, Application US/09040444  
Patent No. 6063766  
GENERAL INFORMATION:  
APPLICANT: Koepsell, Hermann  
APPLICANT: Grundeman, Dirk  
APPLICANT: Gorboulev, Valentin  
TITLE OF INVENTION: Transport protein which effects the  
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flinnagan, Henderson, Farabow, Garrett & Dunner, L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/040,444  
FILING DATE: March 18, 1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: O'Connor, Steven P  
REGISTRATION NUMBER: 41,225  
REFERENCE/DOCKET NUMBER: 2481.1453-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)408-4000  
TELEFAX: (202)408-4400  
INFORMATION FOR SEQ. ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1885 base pairs

	TYPE: nucleic acid	STRANDEDNESS: single	TOPOLOGY: linear	MOLECULE TYPE: DNA (genomic)	US-09-040-444-5
Query Match	8.2%	Score 174.8	DB 3	Length 1885	
Best Local Similarity	48.4%	Pred. No. 5,8e-35			
Matches	612	Conservative	0	Mismatches 637	Indels 15
				Gaps	4
QY	457	ACTGGGGGCACTGGAGCAGAGAGACCTCGGATGGCTGGGAATTGACGACAGACGTCT	516		
DB	407	ACAGGAGGACACCTGGCGGCTGGGCTCCCTCCAGAGATGGCTGGGTCT-----ATGACACGC	460		
QY	517	ACCTGACACCGGCGGACCGAGTGGAGTTCGGATGCGTGGAGGACAACTGGAAGTCCGCC	576		
DB	461	CCGGCTCTTCATCTGCTACCTGATGATTCACACTGGGTGGTGGTGAAGTCTCGGAACTGACC	520		
QY	577	TCACACACCTCCCTGTTCTTCTGATAGGCGCTGCTCGGCTCCCTTCGTGTCGGGACACTGG	636		
DB	521	TCTTTAGCTCTGTTTGAATGGCGGCTCTCTCTTTGGGCTCTCTCGGATGGGTACTTTGG	580		
QY	637	CACACAGGTTTGGGACGAGAAACGTTCTCTTCGGAACCATGCTGTACAGACTGGCTTCA	696		
DB	581	CACACAGGTTTGGGACGAGAAACGTTCTCTTCGGAACCATGCTGTACAGACTGGCTTCA	640		
QY	697	GCTTCTCGACAGATTTTCTCCATCACTGAGTGGAGATGTTCACTGTGTTATTTGTATCGTGG	756		
DB	641	GGCTGCTCAATGGGCTCTTTCGCGCCACATCATGTCATGCTGCTCTTCCGCTGCTGCAGG	700		
QY	757	GCATGGGCGGACATCTCCAACTATGTGGTGAAGCTTCACTACTAGACACAGAAATCTTGGCA	816		
DB	701	GCTGTGTCAGAGGACGACCTGGAAGGCTGCTACACCTCAACACAGAAATTTGTTGCT	760		
QY	817	AGTCAATTTGATTTATTTCTACATATGAGAGTGCACATTTTGTGCGATGGCTATGA	876		
DB	761	CGGGCTCCAGAAAGAGGCTGGGCGATCATGACG---ATGGCTTCACGGATGGGCTGG	817		
QY	877	TGCTGCTGCCACTGTTTGCTTACTTCATCAGAGACTGGGGAAGTCTGCTGGCGCTGA	936		
DB	818	TGGCGGCTTACCGGGCTGGGCTACAGCCGCTGCTCACTGGCGCTGACGCTGGCAGTCT	877		
QY	937	CGGTGGCGGGAATGCTGTGTGTGTCGCCGCTGGGCTGTCATTCGTGAATCCGCCGATGGC	996		
DB	878	CCCTGGCCACCTTCTCTTCTCTGCTCTACTACTGTGTGTGTCGGAGATCCCTCGGTGGC	937		
QY	997	TGATATCCGAGAGAAATTTAGAGAGGCTGAAGATATCATCAAAAAGCTGCAAAAATGA	1056		
DB	938	TGTTATCACAAAAAGAAACACTGAGAGCAATTAAGATATGAGCCACATCGCTCAAAAAG	997		
QY	1057	ACAAACACAGCTTACCAGCAGTGAATTTGATTTCTGTGGAGGAGCTAAATCCCTGAAAC	1111		
DB	998	ATGGGAGTGGCTCTCTCTGATTTTAAAGATGCTTCCCTCGAAGAGGATGTCACGAAA	1057		
QY	1117	AGCAGAAAGCTTTCATCTCGAGCACTGTTCAAGCACTGCGAATATGGCATATGACACATTA	1176		
DB	1058	AGCTGAGGCGCTTCATTTGCAACACTGTTCCGACAGCGCGCCCTGAGAGAGCCACCTTCA	1111		
QY	1177	TGCTTTTGTGCTATGATGCTGACCTCACTGAGGTTACTTGTCTGTCTCTGTGATGCTC	1236		
DB	1118	TCTGTATGACTGTGTGTTACAGGACCTGCTGTCTATACAGGGGCTCATCTACGACATGG	1177		
QY	1237	CTAATTTACATGGAATGCTACCTACCTGAAAGCTTTCCCTCTGCTGATTTGAATTTCCAG	1296		
DB	1178	GGGCGCACAGGCGGAACTCTACTCGATTTCTTTACTCTGCTGTGTCGAAATCCGG	1237		
QY	1297	CTTACATTACAGCCTGCTGCTATTTGGAAAGCTGCGCAAGCGTTATATCATAGCTGAC	1356		
DB	1238	GGGCGCTTATAGCCTCATACCAATGACCGCGTGGGCGGACATACCCCATGGCGGT	1297		
QY	1357	TACTGTTCTGGGAGAGAGTGTGCTTCTTCACTTCACTGCTGACTGTGATTTTACT	1416		
DB	1298	CAAAATTTTGTGGCGGGGACACCTGCTGCTGCAATTTTATCTCACT---GACCTGCACT	1354		





## RESULT 8

US-08-647-397-1

; Sequence 1, Application US/08647397

; Patent No. 5972702

; GENERAL INFORMATION:

; APPLICANT: Belier, David R.

; APPLICANT: Brady, Kevin P.

; TITLE OF INVENTION: OSTEOCLAST TRANSPORTER

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wolf, Greenfield &amp; Sacks, P.C.

; STREET: 600 Atlantic Avenue

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/647.397

; FILING DATE:

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Gates, Edward R.

; REGISTRATION NUMBER: 31,616

; REFERENCE/DOCKET NUMBER: B0801/7048

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-720-3500

; TELEFAX: 617-720-2441

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2102 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHEICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: Internal

; ORIGINAL SOURCE: Internal

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 120..1733

; US-08-647-397-1

; Query Match

; Best Local Similarity 44.5%;

; Pred. No. 1.2e-17;

; Matches 538; Conservative 0;

; Mismatches 650; Indels 21;

; Gaps 2;

; Score 107; DB 2; Length 2102;

; DB 2; Length 2102;

; DB 2; Length 2102;

; DB 2; Length 2102;

; DB 2; Length 2102;

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; DB 2; Length 2102;

; DB 2; Length 2102;

; DB 2; Length 2102;

; DB 2; Length 2102;

; DB 2; Length 2102;

; DB 2; Length 2102;

QY 824 TCGATATATCTCTACATAGAGTGTGCACATTTTTCAGTGTGCTATATCTGT 883

DB 737 GCGGCGCATCTCATACACAACTATTTGGTAC---TGTACACCAATTTGGTACATCTCT 793

QY 884 GCCACTGTTGCTTACTTATCATAGAGTGTGCGGATGCTGCTGCGCGCTGACAGTGTCC 943

DB 794 GCGTGGCTGCGCTATGCGCTTCTCATAGTGTGCGGATGCTGCTGCGCGCTGCTGCTG 853

QY 944 GGGAGTGTGTGTGCGCGCTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1003

DB 854 CTTCCTCATCTCTCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 913

QY 1004 CCAGAGAGATTTAGAGAGCTGAGAGATTCATCCAAAACCTGCAAAAATGAAACACAC 1063

DB 914 GTCTGGAATTTCTCAGAGCTGAGAGACCTGAGAGACCTGAGAGACCTGAGAGACCT 973

QY 1064 AGCTGACAGAGATGATATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1121

DB 974 GAAG 1093

QY 1122 -----AAGCTTCAATCTGAGAGCTGTTCAAGAGCTGAGAGAGAGAGAGAGAG 1165

DB 1034 CACCTGAGCAG 1093

QY 1166 AATGACCATTTATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1225

DB 1094 TGTGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153

QY 1226 TCTGAGTCTCTAATTTACATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1285

DB 1154 TATGAG 1213

QY 1286 TGAATTCAGAGATTCATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1345

DB 1214 TGCATTTCCCGCAAGATTATCATATCTCTCCATTAATTTATTTGAGAGAGAGAGAGAG 1273

QY 1346 CATAGCTGAG 1405

DB 1274 TCAGAGCTTCTCTGATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1333

QY 1406 GATATTTATCTTATATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1465

DB 1334 AGAATGAG 1393

QY 1466 TTTCTCATGCTATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1525

DB 1394 CTTCAGCTGCT 1453

QY 1526 GGTGGGGGACATGACAG 1585

DB 1454 TATGGGTATCATATATGAG 1513

QY 1586 CCTGCTGCTTACACAG 1645

DB 1514 CACGGAG 1573

QY 1646 TGAATCTTACAG 1705

DB 1574 AGGAG 1653

QY 1706 GCAGATGCA 1714

DB 1634 GCAGATGCA 1642

RESULT 9

US-08-592-126-108/c

; Sequence 108, Application US/08592126

; Patent No. 5821091

; GENERAL INFORMATION:

; APPLICANT: Gregory Dolganov

; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory

; Polypeptides

; TITLE OF INVENTION: Polypeptides

```

NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G78.seq
US-08-592-126-108

Query Match 4.9%; Score 104; DB 1; Length 370;
Best Local Similarity 76.2%; Pred. No. 3e-17;
Matches 128; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Y 641 CAGGTTGGCGAGGAACGTTCTCTTCGCAACCATGGCTGTACAGATGGCTTCAGCTT 700
D 221 CAGGTTGGCGAGGAATGTGCTGTTCGACCATGGCGCTGCGACAGAGCTTCAGCTT 162
Y 701 CCTCAGATTTTCTCCATCAGCTGGAGATGTCAGTGTGTTATTTGCATCGTGGCAT 760
D 161 CCTCAGACCTTCGCGAAGATTTTGAATTTGTGTCGTGCTGTTGCTTGTGAGCAT 102
Y 761 GGGCCAGATCTCCAACTATGTGTGTAAGCCTTATCTAGCAACAGAAAT 808
D 101 GGGCCAGATCTCCAACTATGTGGGAGCAGCATTTGTCTCTGGTATGGCCAT 54

RESULT 10
US-08-592-126-109
; Sequence 109, Application US/08592126
; Patent No. 5821091
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 481 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: H993.seq
US-08-592-126-109

Query Match          4.9%; Score 104; DB 1; Length 481;
Best Local Similarity 76.2%; Pred. No. 3,4e-17;
Matches 128; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY      641 CAGGTTGGCAGGAAGAAGACTTCTCTCCACCAACAGCGGTGCAGACGCTTCAGCTT 700
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DB      169 CAGGTTGGCGGGAAGAATGCTGTTCCGCCCATGGCAGCAGACAGGCTTAGCTT 228
        |||||||

OY      701 CCTCAGATTTTCCATCAGCTAGCGGAGATGTTCACTGTTATTGTCATGTTGGGAT 760
        |||||||
DB      229 CTCGACATTTCTCCAGAGAAATTTTGAGATGTTTGTGCGTGCTGTTGCTCTGTAGGCAT 288
        |||||||

OY      761 GGCCAGATCTCCAACTANGTGGTAGCCTTCATCTAGAACAGAAAT 808
        |||||||
DB      289 GGCCAGATCTCCAACATATGTGGCAGCAATTTGTCGGGTANGGCAT 336
        |||||||

RESULT 11
US-09-572-147-1
; Sequence 1, Application US/09572147
; Patent No. 6420544
GENERAL INFORMATION:
APPLICANT: Lin Yue
APPLICANT: John Fieid
APPLICANT: Hanna Ellens
TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: ENCODING MURINE ORGANIC ANION TRANSPORTER 5 (MOATP5) AND
TITLE OF INVENTION: SCREENING METHODS THEREOF
FILE REFERENCE: GP-70622
CURRENT APPLICATION NUMBER: US/09/572,147
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 60/134,879
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1638
TYPE: DNA
ORGANISM: MUS MUSCULUS
US-09-572-147-1

Query Match          4.1%; Score 87.6; DB 4; Length 1638;
Best Local Similarity 43.9%; Pred. No. 9,2e-13;
Matches 554; Conservative 0; Mismatches 679; Indels 29; Gaps 3;

OY      477 GAGAGCTGCTCGAATGGCTGGGAGTTTACGACAGAGACTTACTGTCCACCGCTGAGACC 536
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Db 1475 TGGCGGCGCTACGAGGAGGAGTGGAGGAGCGCCGCCACCGGGGCGCTCTCTCGG 1534  
QY 307 AGCGCGGCGAAGCTGAGCAGCGCGCTGGCGCAACAGTGTCCGCTGGCGGCTGCGGAGC 366  
Db 1535 AGAGGCTCATGGAACCTCTTAAGCGCTTGAAGGAGGAGGAGAGAGCTCTTTGGCTCT 1594  
QY 367 GCCGCGAGTGGCCCAACAGCTGAGCGGCTGCGCAGCATCGCCAACTTCTCGG 426  
Db 1595 ACCACGAGGTGAAAAAGCCCTCTCCGGGCTCTGGCCCAATGAGAGCCACCGGGGTAC 1654  
QY 427 CGCTGGGCTGAGCGCGGGCGCGAGCTGAGCTGGGCGAGCTGGAGGAGAGAGCTGCC 486  
Db 1655 GGGTGGAGCTGGCTTACCTGAGCGCTTCCCTGAGCTTGGAGGAGATCCCGCGC 1714  
QY 487 TGGATGGCTGGAGTTCAGCAGAGCTTACCTGCTCCACCGCTGAGCGAGTGAATC 546  
Db 1715 TCGAGAGAGAGGTCTTCGCTTGGGCGGCGCACCCCTCAACTCAACTCCGGGAGCAGC 1774  
QY 547 TGGTGTGAGGACAACTGGAAGGTGCCCTCACCACCT 585  
Db 1775 TGGAAAGGGTGTCTTTGACGAGCTTAGGCTTCCGCGCT 1813

RESULT 15  
PCT-US95-15327-1  
Sequence 1, Application PC/TUS9515327

GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Biologically Active Fragments of  
TITLE OF INVENTION: Thermus Flavus DNA Polymerase  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15327  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaas, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE//DOCKET NUMBER: 28003/31716  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3048 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 301..2805  
PCT-US95-15327-1

Query Match 2.68; Score 55; DB 5; Length 3048;  
Best Local Similarity 46.13; Pred. No. 0.00025;  
Matches 184; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY 187 GGGGGCCCTCCAGCGGCTATCTTCTGCTGAGCGGAGATCAATCCCAATGGCT 246  
Db 1415 GGGAGACCCATGCTCTCGCTACCTCTGAGACCCCTCAACACACCCCGAGGGG 1474

QY 247 TCAATGATATGTCAGTCTGTTCTCTGCGGAGAACCCGAGCAACCGCTGTCAGTGCAGG 306  
Db 1475 TGGCGGCGGCTTACGAGGAGGAGTGAACGAGAGACGCGCCGCCACCGGCGCTCTCTCGG 1534  
QY 307 AGCGCGGAGAACCTGAGCAGGCGCTGGCGCAACAGTGTCCGCTGGCGGCTGCGGAGC 366  
Db 1535 AGAGGCTCATGGAACCTCTTAAGCGCTTGAAGGAGGAGGAGAGAGCTCTTTGGCTCT 1594  
QY 367 GCCGCGAGTGGCCCAACAGCTGAGCGGCTGCGCAGCATCGCCAACTTCTCGG 426  
Db 1595 ACCACGAGGTGAAAAAGCCCTCTCCGGGCTCTGGCCCAATGAGAGCCACCGGGGTAC 1654  
QY 427 CGCTGGGCTGAGCGCGGGCGCGAGCTGAGCTGGGCGAGCTGAGCAGAGAGAGCTGCC 486  
Db 1655 GGGTGGAGCTGGCTTACCTGAGCGCTTCCCTGAGCTTGGAGGAGATCCCGCGC 1714  
QY 487 TGGATGGCTGGAGTTCAGCAGAGCTTACCTGCTCCACCGCTGAGCGAGTGAATC 546  
Db 1715 TCGAGAGAGAGGTCTTCGCTTGGGCGGCGCACCCCTCAACTCAACTCCGGGAGCAGC 1774  
QY 547 TGGTGTGAGGACAACTGGAAGGTGCCCTCACCACCT 585  
Db 1775 TGGAAAGGGTGTCTTTGACGAGCTTAGGCTTCCGCGCT 1813

Search completed: July 5, 2003, 07:07:36  
Job time : 99 secs

Db 222 CTTACCGGCTGTCTCCGTGTTCTGATAGCGACCCCGGAGCACCGCTGCCGGGTGCC 28

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QY 305 GGACCGCGAAGCTGAGACAGCGCTGCGCCAAACAGAGTCCCGCTGCGGCTGCGGGA 364
Db 282 GGAGCGCGCGAAGCTGAGACAGCGCTGCGCCAAACAGAGTCCCGCTGCGGCTGCGGGA 341
QY 365 CGGCGCGAGAGTGGCCCAAGCTGACAGCGCTGACCGGCTGCGCCAGCATGCGCAACTTCTC 424
Db 342 CGGCGCGAGAGTGGCCCAAGCTGACAGCGCTGACCGGCTGCGCCAGCATGCGCAACTTCTC 401
QY 425 GGCCTGCGGCTGAGAGCGCGGCGCGAGCTGAGAGCTGGGCGAGCTGGAGAGAGCTG 484
Db 402 GGCCTGCGGCTGAGAGCGCGGCGCGAGCTGAGAGCTGGGCGAGCTGGAGAGAGCTG 461
QY 485 CTTGATGCTGGAGAGTTCAGCCAGAGCTGCTACCTGCTCCAGCGTGTGAGAGAGTGA 544
Db 462 TCTGATGCTGGAGAGTTCAGAGAGCTGCTACCTGCTCCAGCATGCTGAGAGAGTGA 521
QY 545 TCTGATGCTGAGAGAGTTCAGAGAGTGGCCCAAGCTGCTGCTGCTGCTGCTGAGCGT 604
Db 522 CTTGATGCTGAGAGAGTTCAGAGAGTGGCCCAAGCTGCTGCTGCTGCTGCTGAGCGT 581
QY 605 GCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 664
Db 582 GCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
QY 665 CTTGCGAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 724
Db 642 GTTGTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 701
QY 725 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 784
Db 702 TGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 761
QY 785 AGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 844
Db 762 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 821
QY 845 AGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 904
Db 822 AGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
QY 905 CAGAGAGTGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 964
Db 882 CCGAGAGTGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941
QY 965 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
Db 942 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1001
QY 1025 TGAAGATATCATCAAAAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1084
Db 1002 AGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1061
QY 1085 TGAATGCTGAGAG-----GAGCTAATCCCTGAGAGAGTGGAGAGTGGAGAGTGG 1138
Db 1062 TGACCGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 1121
QY 1139 CCGTGTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 1198
Db 1122 TCGCTGCTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGT 1181
QY 1199 GAGCTGAGTGGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 1258
Db 1182 CATATGAGTGGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 1241
QY 1259 CCTGAAGTGGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 1318
Db 1242 TGAAGTGGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1301
QY 1319 ATGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGT 1378
Db 1302 GCTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGT 1361
QY 1379 GCTTCTCTCATTCAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1438
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Db 1362 CCTTCTCTCATTCAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1421
QY 1439 GCTGAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1498
Db 1422 GGTGAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1481
QY 1499 CTACCCAAAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1558
Db 1482 GTATCCACAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1541
QY 1559 CAGCATGATGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGT 1618
Db 1542 CAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1601
QY 1619 GCTGATGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1678
Db 1602 TCTCATGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1661
QY 1679 GGAATGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1738
Db 1662 CGGTACCCAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 1721
QY 1739 GAAAAAAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 1776
Db 1722 AAAAAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGTGG 1759
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## RESULT 2

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US-09-798-743A-4
; Sequence 4, Application US/09798743A
; Patent No. US2002099093A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-ichi
; APPLICANT: Ose, Asuka
; TITLE OF INVENTION: SYSTEMIC CARNITINE DEFICIENCY GENE AND USES THEREOF
; FILE REFERENCE: 06501-073001
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/JP99/04853
; PRIOR FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: JP 10-252683
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1888
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (60)..(1730)
US-09-798-743A-4
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Query Match 46.6%; Score 994; DB 10; Length 1888;  
Best Local Similarity 75.7%; Pred. No. 1.9e-295;  
Matches 1247; Conservative 0; Mismatches 395; Indels 6; Gaps 1;

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QY 130 GAGGCGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 189
Db 43 GGGAGGCTGAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 102
QY 190 GGGCTTCCAGAGGCTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 249
Db 103 GGGCTTCCAGAGGCTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 162
QY 250 ATGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 309
Db 163 ATGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 222
QY 310 CCGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 369
Db 223 CCGTGAAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGG 282
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QY	370	GGAGATGGCCCCACAGTCTCACCGCTTACGGCTGGCCACCAATGCAACTTCTGGGCC	429
Db	283	GACAGGTGCTCAGAAATATCCGCGCTACCCAGCTGGCCACATCCGCAACTTCTCGAGC	342
QY	430	TGGGGCTGGAGCCGGGGCGCAGCGTGACCTGGGGCAGCTGGAGCAGAGCTGGCTGG	489
QY	430		489
Db	343	TAGGCTGGAGCCGGGGCGGAGCGTGACCTGGAGCAGCTGGAGCAGAGACTGGCTGG	402
QY	490	ATGGCTGGGAAATTCAAGCCAGAGCGTCTACTGTCCACCGCTCGTGACCCGAGTGGAAATCTGG	549
Db	403	ATGGCTGGGAGTACGCAAGAGAGCGTCTTCTGTCCACCAATCGTAGCAGAGTGGAGACTGG	462
QY	550	TGTGTAGAGACAACTGGAAGGTGGCCCTACACACCTCCCTGTCTTCTGTAGGCGTGGCC	609
Db	463	TGTGTAGAGATAGCTGGAAAGGCCCACTACACACTCCCTGTCTTCTGTGGGTGGCTGTA	522
QY	610	TGGGCTCTCTTCTGTCCGGGGCAGCTGTCAAGACAGTTTGGCAGAGAAACCTTCTCTTGG	669
Db	523	TGGGCTCTCTTCAATTTAGGACACCTCTCAGACAGGTTTGGTGCAAGAAATGTGCTCTTTT	582
QY	670	CAACCAATGGGTGACAGAGCTGGGCTTACGCTCCCTGAGATATTTCTCCATCAGCTGGGAGA	729
Db	583	TGACCAATGGGACATGCAGACTGGCTTACGCTTCTCGAGGCTCTTCTGTGGAATTTGAGA	642
QY	730	TGTTCACTGTGTATTTGTATCGTGGGCAATGGGCGACATCTCCAACTATGTGTAGCCT	789
Db	643	TGTTTACAGGCTTTTGTTCCTGTGTGGCATGGGTGACAGATCTTCAACTACGTGGCAGCAT	702
QY	790	TCTACTAGGAACAGAAATCTTGGCAAGCACTTGGTATATCTGTACACTTATTTGGAG	849
Db	703	TCTCTCCGGGAACAGAAATCTTCCAAAGCAATATGGAATTAATTTGGCCACTTTAGGAG	762
QY	850	TGTGCACATTTTGTGCAAGTTGCGTATATGCTGTGCGACATGTTTGTACTTACTATCAGAG	909
Db	763	TTTGCAATATTTTATAGCGTTTGCGTTATGGTGTGCGACACTGTTTGCACTACTTATCATAGAG	822
QY	910	ACTGGCGGAGTGTGTGTCTGTGGCGCTGACGCTGCCGGGAGTGTGTGTCTGCCCTGTGT	969
Db	823	ACTGGAGAGTGTGTGTCTGTGGCGCTCACTGTGCGAGGGGTGTATGTGGGGCTCTCGGT	882
QY	970	GGTTTCATTCCTGGAATCTCCCGGAGGCGTGATATCCAGAGAAATTTAGAGAGGCTGAAG	1029
Db	883	GGTTTACCTCTGAGTCTCCCAACGATGCTGTCTCTCAAGGCCCAATTAAGAGGCGAGG	942
QY	1030	ATATCATCAGAAAAAGCTGCAAAAAATGAACAACAAGCTGTACAGCAGATATTTGATT	1089
Db	943	TGATCATCCCAAGAAAGCTGCCAAATCAATAGGGAATTTGTGCACCTTCCACTATCTTCGATC	1002
QY	1090	CTGTGGAG-----GACCTAAATCCCTGAAAGCAGCAAGAAAGCTTTCATCTGGACCTGT	1143
Db	1003	CAAGTGTATTCAGAGACTTAAATTTACGAAAGCTCAGTTGACACCACTATTTATGATGTGA	1062
QY	1144	TCAGAGCTGGGAATTTGCAATATATGACCAATATATGTTTGTCTGTCTGTGGATGCTGACCT	1203
Db	1063	TCGCAACACGGAATATCAGGGTATATCAACATCAATGCTATTAATATCTGTGGGTGACATAT	1122
QY	1204	CAGTGGTACTTGTCTGTCTGTGTGATGCTCTTAATTTACATGAGAGATGCTACTGTA	1263
Db	1123	CAGTGGCTATTTTGGACTATCTTCTTACACTCTTAAGCTTGCAGGGGAGACATATATGTA	1182
QY	1264	ACTTTTTCCTCTGCGCTTGATTAATAATTCAGATTACATTAACAGCTCGGCGTATATGC	1323
Db	1183	ACTTCTTCTACTGTCGGCGGTGTTAAGTCCAGCGTATGTCTGTGGCTGTGTGTGTTC	1242
QY	1324	GAAAGCTGCCAGGCGTTATATATCATATGACTGCATGTCTGTGGGAGAGAGTGTGCTTC	1383
Db	1243	AGTACTTGCCTCCGCGGATATCTATCTGCGCTGCGCTTCTCTGGGTGGCAGTGTCTCTTC	1302
QY	1384	TCTTCAATTCACGTGTACCTGTGGATATATTAATCTTATACATATGATGTGTCTGATGCGGG	1443
Db	1303	TCTTATGACACTGTGTGCTTCAACAAATTTGTTTACTGTGTCCAGTCCCTGTGTATGTGG	1362

[illegible]

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? NAME/KEY: intron
? LOCATION: (14565)..(15590)
? NAME/KEY: exon
? LOCATION: (15591)..(15762)
? NAME/KEY: intron
? LOCATION: (15763)..(17282)
? NAME/KEY: exon
? LOCATION: (17283)..(17409)
? NAME/KEY: intron
? LOCATION: (17410)..(19178)
? NAME/KEY: exon
? LOCATION: (19179)..(19279)
? NAME/KEY: intron
? LOCATION: (19280)..(20947)
? NAME/KEY: exon
? LOCATION: (20948)..(21162)
? NAME/KEY: intron
? LOCATION: (21163)..(22690)
? NAME/KEY: exon
? LOCATION: (22691)..(22873)
? NAME/KEY: intron
? LOCATION: (22874)..(23934)
? NAME/KEY: exon
? LOCATION: (23935)..(24070)
? NAME/KEY: intron
? LOCATION: (24071)..(24443)
? NAME/KEY: exon
? LOCATION: (24444)..(25871)
US-09-798-743A-5

Query Match 17.0%; Score 363.8; DB 10; Length 25871;
Best Local Similarity 92.3%; Pred. No. 4,7e-100;
Matches 383; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 125 TTTCGAGGCGGAGTGGGAGCATGCGGAGCTAGGAGCATGAGTATCGCTTCTTGCGGGA 184
DB 200 TCTGTGGGCTCTTGAGGGGGCGATCGGGACTACGACGAGGACCGCTTCTTGCGGGA 259
QY 185 GTGGGGGCTTCGACGCGCTCATCTTCTCTGCTCAGCGCCAGCATCATCCCAATGG 244
DB 260 GTGGGGGCTTCGACGCGCTCATCTTCTCTGCTCAGCGCCAGCATCATCCCAATGG 319
QY 245 CTTCAATGTATGTCAGTGCCTGCTTCTTGCGGAGACCCCGGACCCGCTGTGAGTCC 304
DB 320 CTTCAAGCGGCTGTCTCTCGCTTCTGATGCGACCCCGGAGCACCGCTGTGAGTCC 379
QY 305 GGACGCCGGAACCTGAGCAGCGCTGCGGACAAACAAAGTTCGCGTGGCGGTGGGGA 364
DB 380 GGACGCCGGAACCTGAGCAGCGCTGCGGACAAACAAAGTTCGCGTGGCGGTGGGGA 439
QY 385 CGGCGCGGAGTGGCCCACTGACGCGCTACCGGCTGCCGACATCGCAACTTCTC 424
DB 440 CGGCGCGGAGTGGCCCACTGACGCGCTACCGGCTGCCGACATCGCAACTTCTC 499
QY 425 GCGCGTGGGTGGAGCCGGGGCGGACGCTGGACCTGGGAGGCTGGAGAGAGAGTG 484
DB 500 GCGCGTGGGTGGAGCCGGGGCGGACGCTGGAGGCTGGAGAGAGAGAGTG 559
QY 485 CCTGAGTGGCTGGAGATTACGACGAGAGCTGTACTCTGTCCAGCGTGTGACCGAG 539
DB 560 TCTGAGTGGCTGGAGATTACGAGAGCTGTACTCTGTCCAGCGTGTGACCGAG 614

RESULT 5
US-09-284-320-30
? Sequence 30, Application US/09284320
? Publication No. US20030092175A1
? GENERAL INFORMATION:
? APPLICANT: Kato, Seisui et al.
? TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
? FILE REFERENCE: GIN-6705CPUS
? CURRENT APPLICATION NUMBER: US/09/284,320

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Db 538 TCTTTCAGTCTCTGTTTAAATGCGGGCTTCTTCTTGGCTCTCGGTGTTGCTACTTTG 597  
QY 637 CAGACAGTTTGGCAGGAGAGAGCTTCTTCCAAACCATGCTGATACAGCTGGCTCA 696  
Db 598 CAGACAGTTTGGCAGGAGAGCTGTTCTCTGGAGAGCTGCTGAGCAAGCGGTCTCGG 657  
QY 697 GCTTCTGAGCAATTTCTCATCATGCTGGAGATGTTCACTGTTATTTGTCATCTGTG 756  
Db 658 GCGTGTCTATGCGCTTCTCGCCCACTACATGTCATGTCAGTCTTCCGCTCTCTCAGG 717  
QY 757 GCATGGGCGGAGTCTCCAACTATGCTGATGCTTCACTAGCAACAGAAATCTTGGCA 816  
Db 718 GCTTGTGTCAGCAAGGAGAGCTGATGCTGCTACACCTCATACAGAAATTTGTTGGCT 777  
QY 817 AGTCAGTTCTATTAATTTCTACATTAAGAGTGTGACATTTTGGAGTGGCTATA 876  
Db 778 CCGGCTTCAGAGAGAGAGGTGGCATATGATACAG---ATGGCTTCAGGGTGGGCTGG 834  
QY 877 TGTGCTGCTGACCTGTTTGTCTTACTTATCAGAGACTGGCGGATGCTGCTGGCGCTGA 936  
Db 835 TGGCGCTTACCGGGCTGGGCTACGCTGCTCAGCGGCTGGGCTGGCTGACAGTGGCTCT 894  
QY 937 CCGTGGCGGAGTGTGTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 996  
Db 895 CCGTGGCGGAGTGTGTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 954  
QY 997 TGAATTCACAGAGAGATTTAGAGAGCTGAGAGATTCATCCAAAAGCTGCAAAAATGA 1056  
Db 955 TGTATTCACAAAAGAGAGAGAGCTGAGAGATTAAGATTAAGAGAGAGAGAGAGAGAG 1014  
QY 1057 ACAGACAGCTGATACAGAGAGATTAATTTGATTTCTGAGAGAGCTAAATCCCTGAGAC 1116  
Db 1015 ATGGAGAGTTGCTCTCTGATTAAGATGCTTCCCTCAAGAGAGTGTACACGAAA 1074  
QY 1117 AGCAGAAAGCTTTCATTTGAGAGCTGCTGAGAGCTGAGAGATTAATGCAATATGACATTA 1176  
Db 1075 AGCTGAGCTTTCATTTGAGAGAGCTGCTGAGAGAGCTGAGAGAGAGAGAGAGAGAG 1134  
QY 1177 TGTCTTGTCTGATGAGATGCTGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTG 1236  
Db 1135 TCTGATGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194  
QY 1237 CTAAATTCATGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1296  
Db 1195 GCGGCAACAGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254  
QY 1297 CTTAATTCATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1356  
Db 1255 GGGGCTTTCATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314  
QY 1357 TACTGCTTGGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1416  
Db 1315 CAATTTGCTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1374  
QY 1417 TCTATTCATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1476  
Db 1375 GGTAAATCAT 1434  
QY 1477 TGTATGCTTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1536  
Db 1435 TGTGCTGCTGAGATGCTGAGCTGATACCCCATATGCTGAGAGAGCTGAGATGAGTGT 1494  
QY 1537 CATCCAGGCTTCCAGAGTGGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1593  
Db 1495 GTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1554  
QY 1594 CTTCACAGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1653  
Db 1555 AGGTCTGCAAGAGCTTGGCTCTCAATTTGTTGGGCTGCTGCTGCTGCTGCTGCTGCTG 1614  
QY 1654 TCACCTTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1713  
Db 1615 TGAGCTTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1674

QY 1714 AGAA 1717  
Db 1675 AGAA 1678  
RESULT 7  
US-10-037-270-271  
; Sequence 271, Application US/10037270  
; Publication No. US20030104529A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenchua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyang  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yundong  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Tillinghast, John  
; APPLICANT: Drmanec, Radoje T.  
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and  
; FILE REFERENCE: Polypeptides  
; CURRENT APPLICATION NUMBER: US/10/037, 270  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1104  
; SOFTWARE: PL-FL-genes Version 1.0  
; SEQ ID NO 271  
; LENGTH: 1865  
; TYPE: DNA  
; ORGANISM: Homo sapiens .  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (107)..(1598)  
US-10-037-270-271  
Query Match 7.18; Score 150.8; DB 9; Length 1865;  
Best Local Similarity 49.38; Pred. No. 3.4e-35;  
Matches 438; Conservative 0; Mismatches 432; Idels 18; Gaps 1;  
QY 856 CATTTTGGAGTGGCTATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915  
Db 567 CTTTGTGAGTGGTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626  
QY 916 GGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 975  
Db 627 GGTTCACAGATGATCTCTCCACAGTACTTCCCTTTATCTGTGCTGTTGGGTGCTG 686  
QY 976 TTTCTGATTCCTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035  
Db 687 TCCAGAGACCTTTTGGCTTCTCTCAGAGGAGAGATGAGAGAGCAAAAATAG 746  
QY 1036 TCCAAAAGCTGCAAAAATGAGACAGAGCTTACAGAGATGATATTTGATTTGATCTGCTG 1095  
Db 747 TTGACATCATAGGCAAGTGGAGAGAGGCAAGCTCTGTAACCTGTGAGACTTTATATAC 806  
QY 1096 AGAGCTAAAT-----CCCTGAGAGAGAGAGAGAGCTTTTCAATCTGCTG 1137  
Db 807 TGGACCTACAGAGTCTCTGTTAGTAATAGCCCTCAGTGAAGTCAAGAGACATATATAT 866  
QY 1138 ACTGTTCAGAGAGCTGGAATATTTGATATATGACATTTATGCTTGTCTGCTGATGAGATGC 1197

Db	Sequence	Length	Accession
Db	ATCTGTTTAACTGAGCAATACGAAAGGACCTTACCGTTTGCGTATCTGGTCA	926	
Db	1198 TGAACCTCAGGAGGTTTACTTGTGCTCTGTCTGTGATGCTCCAAATTTACATGAGAGTCC	1257	
Db	927 CTGGAACTTTGGGATTTCTACTCGTTTCTGTGATTTCTGTAACTTGTAGGAGCAATGAT	986	
QY	1258 ACCTGAACCTTTTCTCTCTGCTTGTATGTAATTCACGCTTACATTACAGCTGAGTGC	1317	
Db	987 ACTTAAACCTCTCTCTCTGCTTGTATGTAATTCACGCTTACATTACAGCTGAGTGC	1046	
QY	1318 TATTGCAAGCGTGGCCAGGCGTTATATCATAGTGTGAGTACGTCTTGTGGGAGGAGGTG	1377	
Db	1047 CCATGACAAAGTGTGGGAGGAGAACAGTCTGTGGCTACTCTCTTTTGTGACGTGCACTGG	1106	
QY	1378 TGGTTCCTTCATTTCAACAGTGTACCTGTGATTTATCTTATTCATTTGCTGTGCTCA	1437	
Db	1107 CCGTGGTGTGCGTTATGTGTATCCGCCAGAAACATTTATTTTGGTGTGTGACAGCTA	1166	
QY	1438 TCGTGGGAAATTTGGGATACCTCTGCTTTCTCCATGCTGTATGTCTTACACTGCTGAGC	1497	
Db	1167 TGGTTGGAAATTTGGCCTGTGGGAGACATTTTGGCCCTCATTTATCTTTAATACAGCTGAGC	1226	
QY	1498 TCTACCCACACCGTGTGAGGAAACATGCGGTTGGGGGTCACATCCAGGCGCTCCAGATGG	1557	
Db	1227 TGTATCCACACATTTGTAAGATCGCTGGCTGTGGGAGCGGAGATGTGTGTGCTGG	1286	
QY	1558 GCAACATCATTTGCCCCCTTACTTTGTTTACTTACCTGTGGTGTCTTACAAACAGATGCTGGCTTACA	1617	
Db	1287 CCAGCATCTGTGGGCGCCCTTCTGTGTGACCTCAGACACATTTGGATCTTCATACACAGT	1346	
QY	1618 TCGTCAATGGGTAGTCTGACTGTCTGTATGTAATCTTACCCCTTTTTCCTGGAAGTT	1677	
Db	1347 TGTGTGTGGGACATGTGGCCCTCTGTGATGGAGTGTAAACATCTTACAGAAACCC	1406	
QY	1678 TGGGAATGACTCTTCCGAAACCTTAGACGAGATGCAAGTGAAT	1725	
Db	1407 TTGGGAACGCGTAGCACTACTTGGGAGGAGGCTGCAAAACCTGGAGT	1454	

	Query Match	6.5%	Score 138	DB 9	Length 1431
	Best Local Similarity	47.3%	Pred. No. 2.5e-31		
	Matches 608	Conservative 0	Mismatches 645	Indels 33	Gaps 5
QY	454	TGACCTGGGGCAGCTGACGACGAGAGACTCCCTGATGCGCTGGGAGATTCACGCCAGACGC			513
Db	2	TGGAGGTGGAGGAGGCGCTTCACGGCGGGGGGAGAGGGCACTCCACCATGATTAATGTGT			61
YY	514	TCACCTGTCACCGCTCGTACCGAGTGTGATTCGTGTGTGAGGACAACTGGAAAGTGC			573

D	b	62	GCCTTCGTCGGCCGTGCTCTCTGACAGGAGTTTAAATYGGCAACAGATTCCTACAAATCA	121
O	y	574	CCCTCACACACCTCCCTCTGTCTGCTGAGACGCTGCCTCCGCTCCCTGCTGCCGGAGC	633
D	b	122	GTGCAGACACTCTTTTCTTCTCAGTGTATTTGTGGAGTATCTCTTTGGTCAGC	181
O	y	634	TGTCAGACAGTTTGGCAGAGAGAACGTTCTCTTCCGACCATAGCTGTACAGACTGGCT	693
D	b	182	TTTTCAGATTCGCTTCGGAAGAAAAAGTCTATCTACACAGGTTTGGCTTGACATCTTAT	241
O	y	694	TCAGCTTCCTCGAGATTTTCTCCATCAGCTGGGAGATGTTCACTGTCTTATTGTCAATCG	753
D	b	242	TTGCAATYGCMAATGAGATTTTCCCTCCATATGATGTTCTTGGCAGTAACCTCGCTCTCGG	301
O	y	754	TGGGCATGGGGCAGATCTCCACATATGTGGAGACTCATACATAGAGAAACAAATTCCTG	813
D	b	302	TGGGCATGATGATGAGAGGATGTGCGTGGTGGCTTTGCTTCTCTTAATGAAATGTGTGG	361
O	y	814	GCAAGTCAGTTCGTATTATATCTCTACATTAGAGATGTGCACATYTTTGTGCAGTTGGCT	873
D	b	362	GCA---CCGCTACTGCGGCACTGTCCAGAGATCGATTGGCGGCGCTCTCTTGCAGATTGGCA	418
O	y	874	ATATGCTGCTGCCACTCTTGTGCTTACTTCAATCAGAGACTGGCGGATCTGCTGTGGCCG	933
D	b	419	TTGGCCCAATATGCCCCCTTATAGAACTACTTCATCCGCTCTGTGAGAGACCTTGACCTTCTGG	478
O	y	934	TGACGGTGCAGGAGTGTGCTGTGTCCCGCTGTGGTGGTTCATCTCGAATCTCCCGAT	993
D	b	479	TTAACTGTCAGAGGAGACGATGTCTCTTCTCTTATCTTTATTCATCTCTGAAATCACTGTGT	538
O	y	994	GGCTGATATCCCAAGAGAATTTAGAGAGCGTGAAGATATCATCCAAAAGCTGCCAAAA	1053
D	b	539	GGTATATCTCCACAGGTCGACTGTAGTGAGGTGAAGAGCGCGCTGTACTCTATGCCAAGA	598
O	y	1054	TGAACAAACACAGCTGTACAGCACTGATTTGATTCTGTGGAGAGACTTAATCCCTGCA	1113
D	b	599	GGAACCCCA--AACTCAAGTGCACCTTCTCACTAACACACCAGCCAAACAGAGGTGAG-	656
O	y	1114	AGCAGCAAGAAAGCTTTCATCTGTGACCGGTTCAGAGCTCGGAATATTTGCCATATGACCA	1173
D	b	657	----GGAGACTGGAAGTTTCTGTGATCTTCTGCTTACCCGGGCTCTGTAGACACACTT	712
O	y	1174	TTATGCTTTGCTGCTATGATGCTGACCTCAGTGGGTACTTGTCTCTGCTCTGCGATG	1233
D	b	713	TGATCCGATGTTCTATCTGTTTGTGTGGCACTTGGTGTATATAGGCCCTAACTGTGAGTG	772
O	y	1234	CTCTTAATTTACATGAGATGCTCACTGAACTGTTTCTCTCTGCTTGTGATTGAAATTC	1293
D	b	773	CGGGTGAATCTAGTGGAAATTTATTTACCAACCTGGCCCTGTGCGCTCATAGAGATTTC	832
O	y	1294	CAGCTTAC---ATTACAGCCGTGGGTGCTATTGGCAACGCTGCCAGGCGTTATATCATAG	1350
D	b	833	CATCTTACCCCTCTCTGTATCTACTTGATTAACCAAAAATGGTTTGTGTGGAGAGCAAT	892
O	y	1351	CTGCAGTACTGTTTGGGAGAGAGTGTGCTTCTTCATTCACATGTAACCTGTGATTT	1410
D	b	893	TATCAGATTTCTGTGCTTAGAGAGACTGGTGTCTATTTGTAATGTTTCTTCCAGAAA	952
O	y	1411	ATTACTTCTTA-----TCCATTTGCTGTGTCATGCTGGGAAAAT	1449
D	b	953	AGAAAGACACAGTGTGTGTTCAGTGTGAACACCACTTCCTTCTGCTGTGGGGAAGC	1012
O	y	1450	TTGGGATCACCTGCTGCTTCTCCATGCTGTAATGTTCTTACAGCTGAGACTCTACCAACCC	1509
D	b	1013	TGACCACTATGCTGCTTTAACATTTTATATATCTTACACCTCTGACCTTTTACCTCTACG	1072
O	y	1510	TGCTCAGGAACATGGCGGTGGGGGTTCACATCCAGGCGCTCCAGATGGGCGAGCATATYG	1569
D	b	1073	TCATCAGGAATGTTGGGCTTGGAACTGTTCCATGTTCTCCCGAGTTGGTGGAGATTATTTG	1132
O	y	1570	CCCCCTACTTGTGTTTACCTGAGTCTTACCAACAGAAATGTGCCCTCATGTCATGGGATA	1629

Db 1133 CTCCTTCATCCCTCACTGAAATATGCGACATGCTTATACATTCATGTCTTCCGAG 1192

Qy 1630 GTCTGACCTGTCTCTATGATGGAATCTTACACCTTTTTCCTCGAAAGTTTGGGAATGACTC 1689

Db 1193 CCACGGGCTCACTCCGCGCTCTCTGTGATTTGTTATTTGCGGAGACCTTAAACGTCCGC 1252

Qy 1690 TTCCAGAAACCTTAGACAGATGCGAG 1715

Db 1253 TGTGAGAAACATTTCTCGACCTTTGAG 1278

RESULT 9  
US-10-15

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Sequence 1, Application US/10155891
Publication No. US20020193585A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Friddle, Carl Johan
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020193585A1 Human Transporter Proteins and Polynucleotides
TITLE OF INVENTION: Same
FILE REFERENCE: LEX-0346-USA
CURRENT APPLICATION NUMBER: US/10/155,891
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/293,710
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1644
TYPE: DNA
ORGANISM: homo sapiens
US-10-155-891-1

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Query Match

Query Match	6.48	Score 136.4	DB 9	Length 1644
Best Local Similarity	47.78	Pred. NO. 8.7e-31		
Matches 583	Conservative 0	Mismatches 606	Indels 33	Gaps 5

QY 518 CTTCTCCACCGTCGTGACCAGATGGAACTCGTGCTGTGAAGGCACAACACTGGAAGTGCCTC 577  
Db 279 CTTCACCTCCACCGCTCGGAGGTGTTTTTAATTGCCAACAGATCTCAAAAAGTAGTGGC 338

QY 578 CACCACCTCCCTGTTCTTCGTAGGCGTGECTCCCTGGCTCTCTGCTGATCCGGGACAGCTTC 637  
Db 339 AGCAAAGCTCTTTTTTCTCACTGGGTATTTGTGGAGTATNCTCTTTTGGCACCTTTC 398

QY 638 AGAAGAAGTTTGGCAGGAAGAACTTCTCTTGCCAACCATGCGCTGTACAGACTGCGCTCAG 697  
Db 399 AГАТСGCTCGGAAGAAAAAGCTATCTCACAAGTTTCTCTTGACACTTATTATTCG 458

QY 698 CTTCCTGGAGATTTTTCCTCATCACTGGAGATGTCTACCTGTATTATTCACCTGGG 757  
Db 459 ААТГССААТАТGAAТТТТТССССТАТАТАGATTTCTTTGСАТАМАССТТТССТТССТТGS 518

QY 758 CATGGGCGAGATCTCCAACTATGTGTAGCCTTCATACTAGGAACAGAAATCTTGSCAA 817  
Db 519 CATGATGATGAGGAGATGTGCGTGGGCCCTTTGTCTGTATAGATGTGGGCAC 578

QY 818 GTCACTTCGATTTATATTTCTTACATTAGAGATGTGCACATTTTTTGGAGTTGGCTATAT 877  
Db 579 CGCCTACTGGGCATCTGCAGGATGATTTGGCG---GCCTCTTCTTTGCAGTTGGCATATGC 635

QY 878 GCTCTCGGCACATGTTTGTCTACTCATCAGACACTGGGGAATGCTGCTGCTGGCGCTAC 937  
Db 636 CCААТТАТGССТТgTТАggATATCTTCATCCGCTCGTGGAGGACCTTAGCCATTTGGTTAA 695

QY 938 GGTCGCGGAGATGCTGTGTGCTCCGCTGTGGTTCTATTCTCTGAATCTCCCAGTGGCT 997  
Db 696 CTCGCAAGGAAGSGTGGCTTCTCTTATCTTTATCTCATTCCTGAATCACTCGTTGGTT 755

QY 998 GAATATCCACAGAAAGATTTAGAGAGGCTGAAGATATCATCCMAAAAAGCTGCAAAAATGAA 1057

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QY	1058	CAACACAGCTGTACACAGCAGTATATTGATTCTGTGGAGAGAGCTAAATCCCTGMAACA	1117
Db	816	CCGGA-AACCTCAAGTGCACGTTCTCACTAACACACCCGCAACGAGAGCTGCAG-----	869
QY	1118	GCACAAGCTTTCATTCTGTGACCGCTTCAGACACTCGGAATATATGOCATATAGACCATAT	1177
Db	870	GGAACTGGAAGTTTCCGTGACATCTTTCGTTACCGGGTCCGTGTAGACACACTTGAT	929
QY	1178	GTCCTTCCTGCTATGATGATGCTGACCTCAGGGGTAACTTTCCTGTGCTCGATGCTCC	1237
Db	930	CCTGATGTCATCTGGTTTGTGTGCAGCTTGATATATGACCTAACTCTGAGTGCAGG	989
QY	1238	TAAATTACNAGAAATGCTACCTGACACTGTTTCCTCTGCTCCCTGTGATGAAATTCACG	1297
Db	990	TGATCTAGGTGGAAGTATTATTATGCAACCTGCGCCTGTCTGACCTCATAGAGATTCATC	1049
QY	1298	TTACATTACAGC---CTGGCTGCTATTGCGAAGCCTGCCAGGGGTATATCATAGCTGC	1354
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Db	1110	AGCAATTCCTGCGCTAGAGAGACGTGGCTGTATTGTAAATGTTCTTCCAGAAAAGA	1169
QY	1415	CTTTTATAC-----CATGTGCTGTATGCTAGGAGGAAAAATTGG	1453
Db	1170	AGACACAGGTGTGTTTGCAAGTGGAACAGCATTCCTGTGCTGTGGGGMAAGCTAC	1229
QY	1454	GATCACTCTGCTTTCATCAGTGTATGTTTACTGTGAGGCTTAACCAACCTGCT	1513
Db	1230	CATGAGTGCCTTTAAATGTTTATATCTATACACCTGAGAGCTTTTAACTTAAGTAT	1289
QY	1514	CAGGAATATGGCGGTGGGGGTCAATCAACAGCGCTCCAGATGTGGGACATCATGGCCC	1573
Db	1290	CAGGAATGTGGGCTTGGAACTGTCTCATATTTCTCCGAGTGGTGGGATTAATGCTCC	1349
QY	1574	CTACTTTGTTTACTCGGTGCTTCAACAGAACTGCGCTACATGCTCATGGTAAGTCT	1633
Db	1350	CTTATATCCCTCACTGAAATATGTGCAATGGTCTTTACATCTATTGTCTTGGAGCCAC	1409
QY	1634	GACTGCTCGTATGGAATCTCACCCCTTTTTCCTGAAAGTGTGGAAATGATCTTCC	1693
Db	1410	GGGTCTAGCCTCGGCGCTCTCGAATTTGTATATCCGAGAGACCTTAACAGTCCGCTGCT	1469
QY	1694	AGAAACCTTGAAGCAGATGCAG	1715
Db	1470	AGAAACATTTCCGACCTTCAG	1491

RESULT 10  
HE-10-155

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US-10-155-891-5
? Sequence 5, Application US/10155891
? Publication No. US20020193585A1
? GENERAL INFORMATION:
? APPLICANT: Walke, D. Wade
? APPLICANT: Friddle, Carl Johan
? APPLICANT: Scoville, John
? APPLICANT: Turner, C. Alexander Jr.
? TITLE OF INVENTION: No. US20020193585A1el Human Transporter Proteins and Polynucle
? TITLE OF INVENTION: Same
? FILE REFERENCE: LEX-0346-USA
? CURRENT APPLICATION NUMBER: US/10/155, 891
? CURRENT FILING DATE: 2002-05-21
? PRIOR APPLICATION NUMBER: US 60/293,710
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 5
? LENGTH: 5166
? TYPE: DNA
? ORGANISM: homo sapiens

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Db 624 CCACCCGTCGCGGGGCGGACACACCTGCTCTCTGACATGATGAGTGAGCGGCGCAG 683  
QY 817 AGTCAGTTCGATATATATCTCTACATTAAGAGTGTGCACATTTTTCAGTGGCTATA 876  
Db 684 GGGCGGACCTTGGTGATGACCTTAACCTCTCTGGGCTTCAGCTCGGCCCATGGGCTTAC 743  
QY 877 TCGTCGTCGACCTGTTTCTTACTTCAATCAGAGACTGGGAGTGGCTGCTGCGCGCTGA 936  
Db 744 AACTGACAG-----TGGCCTACGGGTGCGGAGCTGGACACTGCTGCAGCTGGTGGTCT 796  
QY 937 CGGTGCGGAGAGTGTGTGTGTCCGCGTGTGGTGTATCTGGAATCTCCCGAGATGG 996  
Db 797 CGGTGCGGAGAGTGTGTGTGTCCGCGTGTGGTGTATCTGGAATCTCCCGAGATGG 856  
QY 997 TGTATATCCAGAGAGATTTAGAGAG-----CTGAGATATATATATCC 1038  
Db 857 TCTCTACACACAGGAGCGGTGATTTGGGCGCTGCAGAGAGTGTGAGGGTGGCTCCATCA 916  
QY 1039 AAAAACTGCATAAATGAAACACACAGCTGTACAGCAGTGTATTTGATTTCTGTGAGG 1098  
Db 917 ACGGAAGGGGGGAGTGCAGAGACCTGACCCCTGAGGTCTTGTCTTCAGCATCGGAG 976  
QY 1099 AGCTAATCCCTGGAAGCAGACGAAAGCTTTCAATCTGACCTGTTTCAGAGCTCGGAATA 1158  
Db 977 AGGAGCTGAGCATGGGCGCAGCTCTGCGCAGCTGGGACCTGCTCGCATGCGCGGAC 1036  
QY 1159 TTGCAATATGACATTAATGTCTTGTCTGTATGATGCTGACCTCAGTGGGTTACTTG 1218  
Db 1037 TGGGCTTCCGAGCATTAATCTCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1096  
QY 1219 CTCTGCTGTGATGTGTCTTAATTTATCATGAGATGCTGACCTGGAAGCTGTTCTCTCTG 1278  
Db 1097 GCTTGCGCTGAGACCTGACAGGCGCTGTGGAGACATCTCTCTGCTCCAAATGTTCATTTG 1156  
QY 1279 CCTTGATTAATATTCAGCTTACATTTACAGCTGCTGTGTATGCGAACCTGCGCAGCC 1338  
Db 1157 GTGTGCTGACATCCAGCCAGAGATGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1216  
QY 1339 GTATATATCATGCTGAGTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1398  
Db 1217 GCGCCGAGCTGCGCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1276  
QY 1399 TACCTGTGATTTATTAATCTTATTCATTTGCTGTGTGTGTGTGTGTGTGTGTGTGT 1458  
Db 1277 TGGCCACAGAAATGGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1336  
QY 1459 CTTCTGCTTCTTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1518  
Db 1337 GGGCTGCTTCACTGATCAGTACATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1396  
QY 1519 ACATGGGCGTGGGGGTCACATTCACAGGCTCCAGAGTGGGAGCAGATCATTTGCCCTACT 1578  
Db 1397 TGAAGGAGTGGGCTTGGGCGACATGGGAGAGCCGCTGGAGAGCAGCAGCAGCAGCAG 1456  
QY 1579 TTGTATACCTGCTGT 1638  
Db 1457 TCGGGGCTGTGGGT 1516  
QY 1639 TCTGATTTGGAATCTTACCCCTTTTTCCTGAAGTTTGGGAATGAGCTTTCGAGAA 1698  
Db 1517 TGTGAGTGGCTGGGCGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1576  
QY 1699 CCTTAGAGCAGATCGAGAA 1717  
Db 1577 CCATCCAGATGTGCAGAA 1595

RESULT 12  
US-10-095-139-4  
: sequence 4, Application US/10095139  
: Patent No. US20020165357A1  
: GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.  
APPLICANT: Silos-Santiago, Immaculada  
TITLE OF INVENTION: Millennium Pharmaceuticals, Inc.  
TITLE OF INVENTION: 38554, 57301, and 58324, Human Organic  
FILE REFERENCE: MP101-017P1RM  
CURRENT APPLICATION NUMBER: US/10/095,139  
PRIORITY FILING DATE: 2002-03-11  
PRIORITY FILING DATE: 2001-03-12  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 2866  
TYPE: DNA  
ORGANISM: homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (365)...(2026)  
OTHER INFORMATION: "n" represents ambiguous nucleotides  
NAME/KEY: misc\_feature  
LOCATION: (1)...(2866)  
OTHER INFORMATION: n = A,T,C or G  
US-10-095-139-4  
Query Match  
Best Local Similarity 45.7%; DB 9; Length 2866;  
Matches 585; Conservative 0; Mismatches 665; Indels 29; Gaps 3;  
QY 461 GGGGAGCTGGAGCAGAGAGAGCTGCTGATGCTGTGGAGATTCAGCCAGGAGCTACCT 520  
Db 688 GAGGAGGCGCACAGCAGGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 747  
QY 521 GTCCAGCTGCTGACCGAGT 580  
Db 748 CTCACATCTGTGGCGAATGTGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 807  
QY 561 CACCTCCTGTCTTCTGTAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 640  
Db 808 CCAGGCTATCTACCTGT 867  
QY 641 CAGGTTGGGAGGAGAGAGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 700  
Db 868 CAGGTTGGGAGGAGAGCTGT 927  
QY 701 CTTGACATTTTCTTCATCAGCTGGGAGATTTCACTGTGTGTGTGTGTGTGTGTGTGTGT 756  
Db 928 GGCACGCTGCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 987  
QY 757 GCATGGGCGACATCTCCAACTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 816  
Db 988 CCAGCGCTGCGGGGCTGAAACCTGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1047  
QY 817 AGTCAGTTCGATATATATCTCTACATTAAGAGTGTGCACATTTTTCAGTGGCTATA 876  
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QY 877 TGTGCTGCGACCTGTTTCTTACTTCAATCAGAGACTGGGAGTGGCTGCTGTGGCGCTGA 936  
Db 1108 AACTGACAG-----TGGCCTACGGGTGCGGAGCTGGACACTGTGTGAGTGTGGTGTCT 1160  
QY 937 CGGTGCGGAGAGT 996  
Db 1161 CGGTGCGGAGAGT 1220  
QY 997 TGTATATCCAGAGAGATTTAGAGAG-----CTGAGATATATATCC 1038  
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QY 1039 AAAAACTGCATAAATGAAACACACAGCTGTACAGCAGTGTATTTGATTTCTGTGAGG 1098  
Db 1281 ACGGAAGGGGCGAGTGCAGAGACCTGACCCCTGAGGCTTGTGTTTCAGCATGCGGG 1340







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Db      620 GAGTGAACCTTTGTGTGCTTCATCGGGCTTTCCGGCAGCTGGCCAGTCCCTGTACATG 679
Qy      597 GTAGCGGTGCTCCTCGGCTCTTCGTTCGCGGCAAGCTGCAGACAGGTGTGGAGAGAAG 656
Db      680 GTGGAGTGTCTCTGGAGCCATGSGTGTGCTACCTGGCGGACAGGCTGGCGCGCGG 739
Qy      657 AACGTTCCTTCGCAACCATGGCTGTACAGACTGGCTTCAGCTTCCTCAGATTTTCTGCC 716
Db      740 AAGGTGTGTATCTTAACCTACCTGCAGACAGAGCTGTGGGAACTGTGCAGCCATGCA 799
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 06:39:30 ; Search time 4827 Seconds  
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Searched: 24791104 segs, 12571243825 residues

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Listing first 45 summaries

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6	2135	100.0	2135	75 US-60-313-371-1989	Sequence 1989, Ap
7	2135	100.0	2224	61 US-60-172-373-5723	Sequence 5723, Ap
8	2131.8	99.9	2224	65 US-60-213-360-3396	Sequence 3396, Ap
9	2131.8	99.9	2224	71 US-60-278-258-6685	Sequence 6685, Ap
10	2130.2	99.8	2224	76 US-60-324-185-10739	Sequence 10739, A
11	2130.2	99.8	2166	1 PCT-US02-17456-18	Sequence 18, Appl
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19	1310.6	61.4	2083	19 US-09-521-195B-23	Sequence 23, Appl
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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## ALIGNMENTS

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Sequence 17, Application PC/TUS0217456  
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FILE OF INVENTION: SLIC22as AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE  
TITLE REFERENCE: EX02-086C-PC  
CURRENT APPLICATION NUMBER: PCT/US02/17456  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US 60/296,076  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/328,605  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/357,253  
PRIOR FILING DATE: 2002-02-15  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 17  
LENGTH: 2135  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-17456-17

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APPLICANT: Oku, Asuka			
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FILE REFERENCE: 06501-057001			
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PRIOR FILING DATE: 1998-05-20			
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PRIOR FILING DATE: 1997-09-08			
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Qy 1801 GAAAAAATATCTACCCCATTTGGTGAAGTGAAGAAACAGAAATTAAGACCTTGGAGAA 1860  
Db 1801 GAAAAAATATCTACCCCATTTGGTGAAGTGAAGAAACAGAAATTAAGACCTTGGAGAA 1860  
Qy 1861 ATTCTGTTCCCACTGAATGAGACTGATGATGATGATGATGATGATGATGATGATG 1920  
Db 1861 ATTCTGTTCCCACTGAATGAGACTGATGATGATGATGATGATGATGATGATGATG 1920  
Qy 1921 ATCAAGAAATGCTGCTATACAGTAAATCTGATGATGATGATGATGATGATGATG 1980  
Db 1921 ATCAAGAAATGCTGCTATACAGTAAATCTGATGATGATGATGATGATGATGATG 1980  
Qy 1981 TTTCAAACCAACATTTCTGAGAGTCTCTTACTATTAATTAATTAATTAATTAAT 2040  
Db 1981 TTTCAAACCAACATTTCTGAGAGTCTCTTACTATTAATTAATTAATTAATTAAT 2040

Db 1981 TTTCAAACCAACATTTCTGAGAGTCTCTTACTATTAATTAATTAATTAATTAAT 2040  
Qy 2041 AAGATGCTTTGAAACATCTTTAGTCAAGAGCTGTAATTAATTAATTAATTAATTAAT 2100  
Db 2041 AAGATGCTTTGAAACATCTTTAGTCAAGAGCTGTAATTAATTAATTAATTAATTAAT 2100  
Qy 2101 ATTCCATCATCAATATCTATCCAAATTAATTAAT 2135  
Db 2101 ATTCCATCATCAATATCTATCCAAATTAATTAAT 2135

RESULT 3  
US-09-521-195b-2  
; Sequence 2, Application us/09521195b  
; GENERAL INFORMATION:  
; APPLICANT: Nezu, Jun-ichi  
; APPLICANT: Oku, Asuka  
; TITLE OF INVENTION: TRANSPORTER GENES  
; FILE REFERENCE: 06501-057001  
; CURRENT APPLICATION NUMBER: US/09/521,195B  
; CURRENT FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: JP 10/156660  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: JP 9/260972  
; PRIOR FILING DATE: 1997-09-08  
; PRIOR APPLICATION NUMBER: PCT/JP98/04009  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 33  
; SEQ ID NO 2  
; LENGTH: 2135  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (147)..(1799)  
US-09-521-195b-2

Query Match 100.0%; Score 2135; DB 19; length 2135;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCGCTTCCGCCCCCAATTTCTAAGACCTGCTGCTCCCGGGAAAGTTCTTAATC 60  
Db 1 CCCCCGCTTCCGCCCCCAATTTCTAAGACCTGCTGCTCCCGGGAAAGTTCTTAATC 60  
Qy 61 CTTGGGAGAGCGCCAGCTACAGACACTGCTCTGAGAACGCTGTCATCACCCGATG 120  
Db 61 CTTGGGAGAGCGCCAGCTACAGACACTGCTCTGAGAACGCTGTCATCACCCGATG 120  
Qy 121 CAAGTTTCGAGCGGAGTGGGAGACATGCTGCTGAGAACGCTGTCATCACCCGATG 180  
Db 121 CAAGTTTCGAGCGGAGTGGGAGACATGCTGCTGAGAACGCTGTCATCACCCGATG 180  
Qy 181 GCGAGTGGGGGCGCTTCCAGCGCTCATCTTCTCTCTACAGCCGACATCATCCCA 240  
Db 181 GCGAGTGGGGGCGCTTCCAGCGCTCATCTTCTCTCTACAGCCGACATCATCCCA 240  
Qy 241 ATGGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
Db 241 ATGGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
Qy 301 TGCAGAGCGCCGCAACTGAGCAGCGCTGCGCAACAGATGTCCTGCGGCTG 360  
Db 301 TGCAGAGCGCCGCAACTGAGCAGCGCTGCGCAACAGATGTCCTGCGGCTG 360  
Qy 361 GGGAGCGCGCGAGTGGCCCAACAGCTGACGCGCTACCGGCTGCGCAACT 420  
Db 361 GGGAGCGCGCGAGTGGCCCAACAGCTGACGCGCTACCGGCTGCGCAACT 420  
Qy 421 TCTCGGCGTGGGAGCGCGGCGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 480  
Db 421 TCTCGGCGTGGGAGCGCGGCGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 480



QY	481	GCCTCCGGAATGGCTGGGAGGTTCAAGCCAGACGCTTCACTACCTGTCCACCTGTGTGACCCAGT	540
Db	481	GCCTCCGGAATGGCTGGGAGGTTCAAGCCAGACGCTTCACTACCTGTGTGACCCAGT	540
QY	541	GGAAATCTGAGTGTGTGAGAGACAACTGAAAGAGGCCCTCACACCTCCCTGTCTTCTGATG	600
Db	541	GGAAATCTGAGTGTGTGAGAGACAACTGAAAGAGGCCCTCACACCTCCCTGTCTTCTGATG	600
QY	601	GCCTGCTCCTCGGCTCCTCGTGTCCGGGACGCTGACAGAGGTTTGGCAGGAAGAACG	660
Db	601	GCCTGCTCCTCGGCTCCTCGTGTCCGGGACGCTGACAGAGGTTTGGCAGGAAGAACG	660
QY	661	TTCTCTTCGCAACCATGGCTGTAAAGACTGGCTTCACGCTTCTCAGATTTTCTTCATCA	720
Db	661	TTCTCTTCGCAACCATGGCTGTAAAGACTGGCTTCACGCTTCTCAGATTTTCTTCATCA	720
QY	721	GCTGGGAGATTTTCACTGTGTATTGTTCATCGTGGGAGATGGGACAGATCCCAAGATG	780
Db	721	GCTGGGAGATTTTCACTGTGTATTGTTCATCGTGGGAGATGGGACAGATCCCAAGATG	780
QY	781	TGTTAGCCCTTCATCTAGGAACAGAAAATCTTGGCAAGTCAGTTTCTATTATTTCTCTA	840
Db	781	TGTTAGCCCTTCATCTAGGAACAGAAAATCTTGGCAAGTCAGTTTCTATTATTTCTCTA	840
QY	841	CATTAGGAGTGTGCACATTTTTTGTCACTGTGGCTATTAGTGTCTGCCACTGTTCCTTACT	900
Db	841	CATTAGGAGTGTGCACATTTTTTGTCACTGTGGCTATTAGTGTCTGCCACTGTTCCTTACT	900
QY	901	TCATCAGAGACTGGCGGATGCTGTGTGGGGGCTGAGAGGTCCGGGAGTGTGTGTGCC	960
Db	901	TCATCAGAGACTGGCGGATGCTGTGTGGGGGCTGAGAGGTCCGGGAGTGTGTGTGCC	960
QY	961	CGCTGTGTGTTCATTCTGTGAATCTCCCGGATGGCTGATATCCACAGAAAGATTTAGAG	1020
Db	961	CGCTGTGTGTTCATTCTGTGAATCTCCCGGATGGCTGATATCCACAGAAAGATTTAGAG	1020
QY	1021	AGGCTGAAAGATATATATCCAAAACCTGCAAAAATGAACACACGCTGTACACACTGA	1080
Db	1021	AGGCTGAAAGATATATATCCAAAACCTGCAAAAATGAACACACGCTGTACACACTGA	1080
QY	1081	TATTGGATTCTGTGGAGAGCTTAATCCCTGGAAGCAGCAGAAAGCTTTCATCTGTGGACC	1140
Db	1081	TATTGGATTCTGTGGAGAGCTTAATCCCTGGAAGCAGCAGAAAGCTTTCATCTGTGGACC	1140
QY	1141	TGTTCAAGAGACTCGGAATATTGCCATTAATGACCATTAATGTCTTTGCTGTATGATGTCTGA	1200
Db	1141	TGTTCAAGAGACTCGGAATATTGCCATTAATGACCATTAATGTCTTTGCTGTATGATGTCTGA	1200
QY	1201	CCTAGAGTGGTACTTTTGTCTGTCTGTGATGCTGCTCAATTTACATGAGATGCCATCC	1260
Db	1201	CCTAGAGTGGTACTTTTGTCTGTCTGTGATGCTGCTCAATTTACATGAGATGCCATCC	1260
QY	1261	TGAACTGTTCCTCTCTGTGCTTGTGATGAAATCCAGCTTCATTAACAGCCTCGGTGCTAT	1320
Db	1261	TGAACTGTTCCTCTCTGTGCTTGTGATGAAATCCAGCTTCATTAACAGCCTCGGTGCTAT	1320
QY	1321	TGCGAAGCTGGCCAGGCGTATTATPCATAGTGCAGTACTGTTCGTGGGAGAGAGTGTGTC	1380
Db	1321	TGCGAAGCTGGCCAGGCGTATTATPCATAGTGCAGTACTGTTCGTGGGAGAGAGTGTGTC	1380
QY	1381	TTCTCTTCATTCAACTGGTACCTGTGGAATTAATTACTTCTTATTCCAATTTGTCGTGATGC	1440
Db	1381	TTCTCTTCATTCAACTGGTACCTGTGGAATTAATTACTTCTTATTCCAATTTGTCGTGATGC	1440
QY	1441	TGGGAAAATTTGGGATCACCTGTGCTTTCACATGCTGTATGTCTTACTGTCACTGATGCTCT	1500
Db	1441	TGGGAAAATTTGGGATCACCTGTGCTTTCACATGCTGTATGTCTTACTGTCACTGATGCTCT	1500
QY	1501	ACCCAGACCTTGTGAGAACATATGCGGTGTGGGGTGCACATCCAGGCTCCAGAGTGGGCA	1560
Db	1501	ACCCAGACCTTGTGAGAACATATGCGGTGTGGGGTGCACATCCAGGCTCCAGAGTGGGCA	1560
QY	1561	GCATCATTTGCCCTACTTTGTATTACCTCGGTGCTTACACAGAAATGCTGCCCTACATCG	1620

[illegible]

Db 61 CTTGGGAGGCGCCAGCTACAAAGACACTGTCCTGAGAACGCTGTCAACCCGATGTTG 120  
QY 121 CAATTTTCGAGCGCGAGTGGGAGACATGCGGGACTACGACGAGGTGATGCTTCTCTGG 180  
Db 121 CAAATTTTCGAGCGCGAGTGGGAGACATGCGGGACTACGACGAGGTGATGCTTCTCTGG 180  
QY 181 GCGAGTGGGGCCCTTCAGCGGCTCATCTTTCTTCCGTCAGGGCCAGCATCATCCCCA 240  
Db 181 GCGAGTGGGGCCCTTCAGCGGCTCATCTTTCTTCCGTCAGGGCCAGCATCATCCCCA 240  
QY 241 ATGGCTTCAATGATGATGTCAGTGTCTTCTGCGGGGACCCCGAGACACCGCTGTGAG 300  
Db 241 ATGGCTTCAATGATGATGTCAGTGTCTTCTGCGGGGACCCCGAGACACCGCTGTGAG 300  
QY 301 TGCAGGAGCGCGGCAACCTGAGCAGCGCCCTGGGGCAACACAGTGTCTCCGCTGCGTGC 360  
Db 301 TGCAGGAGCGCGGCAACCTGAGCAGCGCCCTGGGGCAACACAGTGTCTCCGCTGCGTGC 360  
QY 361 GGGAGCGCGCGAGAGTCCCGACAGTGCAGCGCTACCGGCTGCGCACCATCGCCAACT 420  
Db 361 GGGAGCGCGCGAGAGTCCCGACAGTGCAGCGCTACCGGCTGCGCACCATCGCCAACT 420  
QY 421 TCTCGCGCTCGGGCTGGAGCCGGGGCGGACGCTGAGCTGGGGCAGCTGGAGCAGGAGA 480  
Db 421 TCTCGCGCTCGGGCTGGAGCCGGGGCGGACGCTGAGCTGGGGCAGCTGGAGCAGGAGA 480  
QY 481 GCTGCGGATGAGTGGGAGTTCAGCCAGGACGCTACCTGTCCACCGCTGTGACGAGT 540  
Db 481 GCTGCGGATGAGTGGGAGTTCAGCCAGGACGCTACCTGTCCACCGCTGTGACGAGT 540  
QY 541 GGAATCTGTGTGAGAGCAACTGGAAGTGCCTCCACACCTCCCTTCTTCTGTAG 600  
Db 541 GGAATCTGTGTGAGAGCAACTGGAAGTGCCTCCACACCTCCCTTCTTCTGTAG 600  
QY 601 GCGTCTCTCGGCTCTCTTCTGTCGCGGCACTGTGACAGAGTTTGGCAGAGAGAG 660  
Db 601 GCGTCTCTCGGCTCTCTTCTGTCGCGGCACTGTGACAGAGTTTGGCAGAGAGAG 660  
QY 661 TTCTCTCGCAACCATGGTGTGACAGAGCTTCCAGCTTCCGAGATTTTCTCATCA 720  
Db 661 TTCTCTCGCAACCATGGTGTGACAGAGCTTCCAGCTTCCGAGATTTTCTCATCA 720  
QY 721 GCTGGGAGATGTTCTACTGTGTTATTTGTCATGCTGGGCAATGGCCAGATCTCCAACTAG 780  
Db 721 GCTGGGAGATGTTCTACTGTGTTATTTGTCATGCTGGGCAATGGCCAGATCTCCAACTAG 780  
QY 781 TGGAGGCTTCATCTGGAACAGAAATTTCTGGCAAGTCACTGCGATTAATTTCTCTA 840  
Db 781 TGGAGGCTTCATCTGGAACAGAAATTTCTGGCAAGTCACTGCGATTAATTTCTCTA 840  
QY 841 CATTAGAGATGTGACATTTTTTTGCAAGTTGGCTAATAGCTGTGCACTTTTGGCTTACT 900  
Db 841 CATTAGAGATGTGACATTTTTTTGCAAGTTGGCTAATAGCTGTGCACTTTTGGCTTACT 900  
QY 901 TCAATCAGAGACTGGCGGATCTGCTGTGCGCTGACGAGTCCCGGAGATGCTGTGTCTC 960  
Db 901 TCAATCAGAGACTGGCGGATCTGCTGTGCGCTGACGAGTCCCGGAGATGCTGTGTCTC 960  
QY 961 CGCTGTGGTTCATTTCTGGAATCTCCCGGATGGGCTGATATCCCGAGAGAAATTTAGAG 1020  
Db 961 CGCTGTGGTTCATTTCTGGAATCTCCCGGATGGGCTGATATCCCGAGAGAAATTTAGAG 1020  
QY 1021 AGGCTGAAGATATCATCCAAAAGCTGCAAAAATGAAACAACAAGCTGTACCGAGCTGA 1080  
Db 1021 AGGCTGAAGATATCATCCAAAAGCTGCAAAAATGAAACAACAAGCTGTACCGAGCTGA 1080  
QY 1081 TATTTGATTTCTGTGGAGAGCTAAATCCCTGAAGCAGAAAGCTTTTCATTTCTGGACC 1140  
Db 1081 TATTTGATTTCTGTGGAGAGCTAAATCCCTGAAGCAGAAAGCTTTTCATTTCTGGACC 1140  
QY 1141 TGTTCAGAGACTCGGAATATTTGCAATATGACATTAATGCTTTGCTGTATGATGATCTGA 1200  
Db 1141 TGTTCAGAGACTCGGAATATTTGCAATATGACATTAATGCTTTGCTGTATGATGATCTGA 1200

QY 1201 CCTCAGTGGGTACTTTGCTGTCTCTGATGCTCTCTAATTTACATGAGATGCTTACC 1260  
Db 1201 CCTCAGTGGGTACTTTGCTGTCTCTGATGCTCTCTAATTTACATGAGATGCTTACC 1260  
QY 1261 TGAACGTGTTCTCTCTGCTGATTTGAATTCAGCTTACATTTACAGCTGGGCTGAT 1320  
Db 1261 TGAACGTGTTCTCTCTGCTGATTTGAATTCAGCTTACATTTACAGCTGGGCTGAT 1320  
QY 1321 TGCAGACGCTGCCAGGCGTTATATCATAGCTGACATGCTTGGGGAGAGGTGTGC 1380  
Db 1321 TGCAGACGCTGCCAGGCGTTATATCATAGCTGACATGCTTGGGGAGAGGTGTGC 1380  
QY 1381 TTCTCTTCAATCACTGATGCTGATGATATATTTACTTTTCAATGCTGCTGATGCT 1440  
Db 1381 TTCTCTTCAATCACTGATGCTGATGATATATTTACTTTTCAATGCTGCTGATGCT 1440  
QY 1441 TGGGAAATATTTGGATCACTCTGCTTCTCCATGCTGTATGCTTCTACTGCTGAGCTCT 1500  
Db 1441 TGGGAAATATTTGGATCACTCTGCTTCTCCATGCTGTATGCTTCTACTGCTGAGCTCT 1500  
QY 1501 ACCCAACCTGCTCAGGAACATGCGGTGGGGGTCAATCCAGGCTTCCAGAGTGGCA 1560  
Db 1501 ACCCAACCTGCTCAGGAACATGCGGTGGGGGTCAATCCAGGCTTCCAGAGTGGCA 1560  
QY 1561 GATCATGCCCCCTACTTTGTTTACCTCGGTGCTTACAAAGAAATGCTGCCATCATCG 1620  
Db 1561 GATCATGCCCCCTACTTTGTTTACCTCGGTGCTTACAAAGAAATGCTGCCATCATCG 1620  
QY 1621 TCATGGGTAGTCTGACTGTCTGATTTGGAATCTTCAACCTTTTCTCCCTGAAGTTTG 1680  
Db 1621 TCATGGGTAGTCTGACTGTCTGATTTGGAATCTTCAACCTTTTCTCCCTGAAGTTTG 1680  
QY 1681 GAATGACTTTCAGAAACCTTAGAGCAGATGACAAAGTGAATGTTTCAATCTGGGA 1740  
Db 1681 GAATGACTTTCAGAAACCTTAGAGCAGATGACAAAGTGAATGTTTCAATCTGGGA 1740  
QY 1741 AAAAAACAAGACTCAATGAGACAGAAAGAAATCCCAAGTCTTAACTGATCTCT 1800  
Db 1741 AAAAAACAAGACTCAATGAGACAGAAAGAAATCCCAAGTCTTAACTGATCTCT 1800  
QY 1801 GAAAAAATATCTACCCCATTTGGTGAAGTGAAGAAATGAAGCCCTGTGGAGAA 1860  
Db 1801 GAAAAAATATCTACCCCATTTGGTGAAGTGAAGAAATGAAGCCCTGTGGAGAA 1860  
QY 1861 ATTGCTGTTCCTCACTGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1920  
Db 1861 ATTGCTGTTCCTCACTGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1920  
QY 1921 ATCAAGAAATGCTGCTCATACAGTAAACTGTGATGATTTCCAGATTAATGCTTGTCT 1980  
Db 1921 ATCAAGAAATGCTGCTCATACAGTAAACTGTGATGATTTCCAGATTAATGCTTGTCT 1980  
QY 1981 TTACAACAACACATTTCTAGAGAGTCTCTTACTCATTAATTCATTAATAATGATTTGCT 2040  
Db 1981 TTACAACAACACATTTCTAGAGAGTCTCTTACTCATTAATTCATTAATAATGATTTGCT 2040  
QY 2041 AAGATGCTTTGAAACATGTTTGAAGAGTGTCAAGAGTGTGAAATACATTAAGATTAACACTC 2100  
Db 2041 AAGATGCTTTGAAACATGTTTGAAGAGTGTCAAGAGTGTGAAATACATTAAGATTAACACTC 2100  
QY 2101 ATTTCCAAATCATCAAAATACATATCCAAATTAATAAT 2135  
Db 2101 ATTTCCAAATCATCAAAATACATATCCAAATTAATAAT 2135

RESULT 5  
US-60-233-468-1989  
; Sequence 1989, Application us/60233468  
; GENERAL INFORMATION:  
; APPLICANT: Ring, Huijun Z.  
; APPLICANT: Malsen, Gareth  
; APPLICANT: Townley, David

APPLICANT: Morris, MacDonald  
APPLICANT: Valdes, Ana  
TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes  
FILE REFERENCE: GX-0013-2 P  
CURRENT APPLICATION NUMBER: US/60/233,468  
CURRENT FILING DATE: 2000-09-18  
NUMBER OF SEQ ID NOS: 2468  
SOFTWARE: PERL Program  
SEQ ID NO 1989  
LENGTH: 2135  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: GB:AB007448  
US-60-233-468-1989

Query Match 100.0%; Score 2135; DB 67; Length 2135;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCGCTTCGGGCCCCCAATTTCTACAGCCCTGCGCCGCGGGAAGCTTCTAATC 60  
DB 1 CCCCCGCTTCGGGCCCCCAATTTCTAAGCTGCTGCTCCCGGGAAGCTTCTAATC 60  
QY 61 CTTGGGAGAGCCCCAGCTACAGACACTGCTCTGAGAAAGCTGTGATCAACCGTAGT 120  
DB 61 CTTGGGAGAGCCCCAGCTACAGACACTGCTCTGAGAAAGCTGTGATCAACCGTAGT 120  
QY 121 CAAGTTTCGAGAGCGGAGAGTGGAGACATGGGGAGTACAGACAGAGTGTATGCGCTTCG 180  
DB 121 CAAGTTTCGAGAGCGGAGAGTGGAGACATGGGGAGTACAGACAGAGTGTATGCGCTTCG 180  
QY 181 GCGAGTGGGGGCCCCCTTCCAGCCGCTCATCTTCTCTGTCAGGCGCAGATCATCCCA 240  
DB 181 GCGAGTGGGGGCCCCCTTCCAGCCGCTCATCTTCTCTGTCAGGCGCAGATCATCCCA 240  
QY 241 ATGGCTTCAATGGTATGTGATGCTGTCTTCTGCGGGGAGACCCCGAGACACCGCTGTGAG 300  
DB 241 ATGGCTTCAATGGTATGTGATGCTGTCTTCTGCGGGGAGACCCCGAGACACCGCTGTGAG 300  
QY 301 TGGCGGAGCGCGGGAACCTGAGACAGCGCTGCGGCAACAAAGTGTCCCGCTGCGGCTGC 360  
DB 301 TGGCGGAGCGCGGGAACCTGAGACAGCGCTGCGGCAACAAAGTGTCCCGCTGCGGCTGC 360  
QY 361 GGGAGGAGCGCGAGGTGCCCAAGCTGAGCGGCTGACCGGCTGCGCACCATGCGCAACT 420  
DB 361 GGGAGGAGCGCGAGGTGCCCAAGCTGAGCGGCTGACCGGCTGCGCACCATGCGCAACT 420  
QY 421 TCTCGGCGCTCGGGGCTGGAGCCGGGGCGGAGCTGGAGCTGGGGAGCTGGAGCAGAGA 480  
DB 421 TCTCGGCGCTCGGGGCTGGAGCCGGGGCGGAGCTGGAGCTGGGGAGCTGGAGCAGAGA 480  
QY 481 GCTGCGCTGATGCTGGAGTTCAGCCAGAGAGCTTCACTGTCTACACCGCTGTGACCGAGT 540  
DB 481 GCTGCGCTGATGCTGGAGTTCAGCCAGAGAGCTTCACTGTCTACACCGCTGTGACCGAGT 540  
QY 541 GGAATCTGATGCTGGAGTTCAGCCAGAGAGCTTCACTGTCTACACCGCTGTGACCGAGT 540  
DB 541 GGAATCTGATGCTGGAGTTCAGCCAGAGAGCTTCACTGTCTACACCGCTGTGACCGAGT 540  
QY 601 GCGTGTCTCTCGGCTCCTTCTGCTCGGGGAGCTGTGACAGAGTGTGGAGAGAGAG 660  
DB 601 GCGTGTCTCTCGGCTCCTTCTGCTCGGGGAGCTGTGACAGAGTGTGGAGAGAGAG 660  
QY 661 TTCTCTTCGCAACCAATGCTGTACAGAGTGGCTTCACTGTCTGACAGATTTTTCATCA 720  
DB 661 TTCTCTTCGCAACCAATGCTGTACAGAGTGGCTTCACTGTCTGACAGATTTTTCATCA 720  
QY 721 GCTGGAGATGTTCACTGTGTATTTGTGATCGTGGGAGATGGGCGAGATCCCAACTAG 780  
DB 721 GCTGGAGATGTTCACTGTGTATTTGTGATCGTGGGAGATGGGCGAGATCCCAACTAG 780

QY 781 TGTAGCCCTCATACTAGAGAACAGAAATTTCTGGCAGTCACTGATATATATTTCTTA 840  
DB 781 TGTAGCCCTCATACTAGAGAACAGAAATTTCTGGCAGTCACTGATATATATTTCTTA 840  
QY 841 CATTAGAGTGTGACATTTTGTGAGTGGCTATATGCTGCTGCCACTGTGTCTTACT 900  
DB 841 CATTAGAGTGTGACATTTTGTGAGTGGCTATATGCTGCTGCCACTGTGTCTTACT 900  
QY 901 TCATCAGAGACGCGGGGATGCTGCTGGGCGTACAGGCTGCGGGAGTGTGTGCTCC 960  
DB 901 TCATCAGAGACGCGGGGATGCTGCTGGGCGTACAGGCTGCGGGAGTGTGTGCTCC 960  
QY 961 CGCTGTGTGTCTTCACTTCCATATCTCCCGATGAGTATATCCAGAGAGATTTAGAG 1020  
DB 961 CGCTGTGTGTCTTCACTTCCATATCTCCCGATGAGTATATCCAGAGAGATTTAGAG 1020  
QY 1021 AGGCTGAAGATATCTCAAAAAGCTGCAAAAATGACACACAGCTGTACACAGTGA 1080  
DB 1021 AGGCTGAAGATATCTCAAAAAGCTGCAAAAATGACACACAGCTGTACACAGTGA 1080  
QY 1081 TATTTGATTTCTGTGAGAGAGCTAAATCCCGTGAAGCAGACAGAAAGCTTCAATCTGAG 1140  
DB 1081 TATTTGATTTCTGTGAGAGAGCTAAATCCCGTGAAGCAGACAGAAAGCTTCAATCTGAG 1140  
QY 1141 TGTTCAGAGACTCGAATATTTGCAATATGACCATTTATGCTTGTCTGTATGATGCTGA 1200  
DB 1141 TGTTCAGAGACTCGAATATTTGCAATATGACCATTTATGCTTGTCTGTATGATGCTGA 1200  
QY 1201 CCTCAGTGGTACTTCTGCTGTCTGTGATGCTCTTAATTTACATGAGATGCTTACC 1260  
DB 1201 CCTCAGTGGTACTTCTGCTGTCTGTGATGCTCTTAATTTACATGAGATGCTTACC 1260  
QY 1261 TGAATCTTCTCTCTGCTGCTGATTTGAATTTCCAGCTTACATTAACGCTGGCTGAT 1320  
DB 1261 TGAATCTTCTCTCTGCTGCTGATTTGAATTTCCAGCTTACATTAACGCTGGCTGAT 1320  
QY 1321 TGGGAGCGTGGCCAGGCGTTATATCATAGCTGACATGCTTCTGGGAGAGAGTGTGC 1380  
DB 1321 TGGGAGCGTGGCCAGGCGTTATATCATAGCTGACATGCTTCTGGGAGAGAGTGTGC 1380  
QY 1381 TTTCTTCAATCACTGATGCTGATGATTTATTTCAATTTGATTTGCTGCTGCTGCT 1440  
DB 1381 TTTCTTCAATCACTGATGCTGATGATTTATTTCAATTTGATTTGCTGCTGCTGCT 1440  
QY 1441 TGGGAAATTTGGGATCACTCTGCTTCTCATGCTTATGCTTCACTGCTGAGCTCT 1500  
DB 1441 TGGGAAATTTGGGATCACTCTGCTTCTCATGCTTATGCTTCACTGCTGAGCTCT 1500  
QY 1501 ACCCAACCTGTGAGAAACATGGGCGGAGTGCATCAACGAGCTGCAAGTGGGCA 1560  
DB 1501 ACCCAACCTGTGAGAAACATGGGCGGAGTGCATCAACGAGCTGCAAGTGGGCA 1560  
QY 1561 GCATCATGCCCCCTCACTTGTGTACCTCGGCTTCAACAGAAATGCTGCCATCACTG 1620  
DB 1561 GCATCATGCCCCCTCACTTGTGTACCTCGGCTTCAACAGAAATGCTGCCATCACTG 1620  
QY 1621 TCAATGGTATGCTGACTGCTGATTTGAATCTTCACTTCTTCTTCTGCTGCTGCT 1680  
DB 1621 TCAATGGTATGCTGACTGCTGATTTGAATCTTCACTTCTTCTTCTGCTGCTGCT 1680  
QY 1681 GAATGACTTCTCAGAAACCTTGAAGAGATGCAAGAAAGTGAATGTTGATGATCTGGA 1740  
DB 1681 GAATGACTTCTCAGAAACCTTGAAGAGATGCAAGAAAGTGAATGTTGATGATCTGGA 1740  
QY 1741 AAAAACAAGAACATGATGAGAGAGAAAGAAATCCCAAGTGTCTAATCACTGATCT 1800  
DB 1741 AAAAACAAGAACATGATGAGAGAGAAAGAAATCCCAAGTGTCTAATCACTGATCT 1800  
QY 1801 GAAAAAATATCAACCCATTTGCTGAATGAAAAACAAAAATTAAGACCTGTGGAGAA 1860  
DB 1801 GAAAAAATATCAACCCATTTGCTGAATGAAAAACAAAAATTAAGACCTGTGGAGAA 1860  
QY 1861 ATTGCTGTCTCCACTGAATGAGTGAATGATTAACGATTAACCAAAATGAACCTTCT 1920

Db 1861 ATTGGTGTCCACCTAATGAGCTGACGTGAACGATTGACACCAATGAACTTGGCT 1920  
QY 1921 ATCAAGAAATGCTGCTGATACAGTAAACCTCTGATGATTTCTCCAGATATATGTCCTGGCT 1980  
Db 1921 ATCAAGAAATGCTGCTGATACAGTAAACCTCTGATGATTTCTCCAGATATATGTCCTGGCT 1980  
QY 1981 TTCAAAACCAACATTTCTGAGAGTCTCTTACTCATTTATTCATGAAATGAGATTGGT 2040  
Db 1981 TTCAAAACCAACATTTCTGAGAGTCTCTTACTCATTTATTCATGAAATGAGATTGGT 2040  
QY 2041 AAGATGCTTGAAGAAACATGTTAGTCAAGGACTGTTAAATATCATATAAGATTACACTC 2100  
Db 2041 AAGATGCTTGAAGAAACATGTTAGTCAAGGACTGTTAAATATCATATAAGATTACACTC 2100  
QY 2101 ATTTCCAATCATCAAAATACTATCCAAATATAAT 2135  
Db 2101 ATTTCCAATCATCAAAATACTATCCAAATATAAT 2135

## RESULT 6

US-60-313-371-1989

; Sequence 1989, Application US/60313371  
; GENERAL INFORMATION:  
; APPLICANT: Ring, Huijun Z.  
; APPLICANT: Malsen, Gareth  
; APPLICANT: Townley, David  
; APPLICANT: Morris, MacDonald  
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes  
; FILE REFERENCE: GX-0013-5 P  
; CURRENT APPLICATION NUMBER: US/60/313, 371  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 2447  
; SOFTWARE: PERL Program  
; SEQ ID NO 1989  
; LENGTH: 2135  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: GB:AB007448  
US-60-313-371-1989

Query Match 100.0%; Score 2135; DB 75; Length 2135;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCGCTTCGGGCCCCCAATTTCTACAGCTGCTGCTCCCGGGGAACGTTCTAACATC 60  
Db 1 CCCCCGCTTCGGGCCCCCAATTTCTACAGCTGCTGCTCCCGGGGAACGTTCTAACATC 60  
QY 61 CTTGGGAGAGCGCCCGAGTACAAAGACACTGCTCTGGAAGCGCTGTCATCACCCGTAGTTG 120  
Db 61 CTTGGGAGAGCGCCCGAGTACAAAGACACTGCTCTGGAAGCGCTGTCATCACCCGTAGTTG 120  
QY 121 CAAGTTTCGAGAGGAGAGTGGGAGAGATCGGGAGCTACGACAGAGTGAATGCCCTTCGG 180  
Db 121 CAAGTTTCGAGAGGAGAGTGGGAGAGATCGGGAGCTACGACAGAGTGAATGCCCTTCGG 180  
QY 181 GCGAGTGGGGGCGCTTCAGAGCGCTCATCTTCTCTGCTGACGGCGAGCATCATCCCCA 240  
Db 181 GCGAGTGGGGGCGCTTCAGAGCGCTCATCTTCTCTGCTGACGGCGAGCATCATCCCCA 240  
QY 241 ATGGCTTCAATGATATGTCAGTCTGTTCTGCGGGGGAACCCCGAGGACCGCTGTCGAG 300  
Db 241 ATGGCTTCAATGATATGTCAGTCTGTTCTGCGGGGGAACCCCGAGGACCGCTGTCGAG 300  
QY 301 TGGCGAGAGCGCGGAACCTGAGACAGCGCTGCGCGAACAACAGTGTCCCGCTGGCGTGC 360  
Db 301 TGGCGAGAGCGCGGAACCTGAGACAGCGCTGCGCGAACAACAGTGTCCCGCTGGCGTGC 360  
QY 361 GGGAGCGCGGAGAGTGGCCCAAGCTGACGCGGTACGCGGTCCCAACATCGGCACT 420  
Db 361 GGGAGCGCGGAGAGTGGCCCAAGCTGACGCGGTACGCGGTCCCAACATCGGCACT 420

Db 361 GGGAGCGCGGAGAGTGGCCCAAGCTGACGCGGTACGCGGTCCCAACATCGGCACT 420  
QY 421 TCTGCGGCGCTCGGAGCTGAGAGCCGGGCGCGAGTGGAGCTGGGAGCTGGAGCAGAGA 480  
Db 421 TCTGCGGCGCTCGGAGCTGAGAGCCGGGCGCGAGTGGAGCTGGGAGCTGGAGCAGAGA 480  
QY 481 GGTGCGCTGGATGGCTGGGAGATTACAGCAGAGAGCTTACTCTCCACCGTCTGTACCGAGT 540  
Db 481 GGTGCGCTGGATGGCTGGGAGATTACAGCAGAGAGCTTACTCTCCACCGTCTGTACCGAGT 540  
QY 541 GGAATCTGTGTGAGAGACAACCTGAGAGTGGCCCTCACACCTCCCTGTTCTTCGAG 600  
Db 541 GGAATCTGTGTGAGAGACAACCTGAGAGTGGCCCTCACACCTCCCTGTTCTTCGAG 600  
QY 601 GGTGCTCTCTGGGCTCTCTTCTGTTCCGGGAGCTGTACAGAGTGGTGGCAGAGAAGC 660  
Db 601 GGTGCTCTCTGGGCTCTCTTCTGTTCCGGGAGCTGTACAGAGTGGTGGCAGAGAAGC 660  
QY 661 TTCTCTTGCAACCATGGCTGTACAGACTGGCTTCAGCTTCCGAGATTTCTTCATCA 720  
Db 661 TTCTCTTGCAACCATGGCTGTACAGACTGGCTTCAGCTTCCGAGATTTCTTCATCA 720  
QY 721 GCTGGAGATGTTCACTGTGTTATTTGTCATCGTGGCATGGGCGAGATTCACAACTATG 780  
Db 721 GCTGGAGATGTTCACTGTGTTATTTGTCATCGTGGCATGGGCGAGATTCACAACTATG 780  
QY 781 TGGTAGCCTTCACTACTAGGAACAATAATTTCTGGCAGTCACTGTTATTTATTTCTTA 840  
Db 781 TGGTAGCCTTCACTACTAGGAACAATAATTTCTGGCAGTCACTGTTATTTATTTCTTA 840  
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Db 841 CATTTAGAGTGTGACATTTTTCAGTGTGCTATATGCTGCTGCTGCTGCTGCTGCTGCT 900  
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Db 901 TCATCAGAGACTGGCGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
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QY 1381 TTTCTTTCATTAACCTGTGACCTGTGATTTACTTCTTATGCTGCTGCTGCTGCTGCTGCT 1440  
Db 1381 TTTCTTTCATTAACCTGTGACCTGTGATTTACTTCTTATGCTGCTGCTGCTGCTGCTGCT 1440  
QY 1441 TGGGAAAATTTGGGATACCTGCTGCTTCTTCTCATGCTGTATGCTTCTTCTGCTGAGCTCT 1500  
Db 1441 TGGGAAAATTTGGGATACCTGCTGCTTCTTCTCATGCTGTATGCTTCTTCTGCTGAGCTCT 1500



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Db 1136 TATTGATTCGTGGAGAGCTAAATCCCTGAGAGAGAGAAAGTTTCATTCTGGACC 1195
QY 1141 TGTTCAGGACTGGGATTAATGGCATATATGACCTTAATGCTTGTGCTATGAGTGTGA 1200
Db 1196 TGTTCAGGACTGGGATTAATGGCATATATGACCTTAATGCTTGTGCTATGAGTGTGA 1255
QY 1201 CCTCAGTGGGTACTTGTCTGTCTGTGATGCTGCTTAATTAATGAGATGGCTTACC 1260
Db 1256 CCTCAGTGGGTACTTGTCTGTCTGTGATGCTGCTTAATTAATGAGATGGCTTACC 1315
QY 1261 TGACCTGTTTCTCTGTCTGTGATGAATTCACAGCTTACATTAACAGCTGCTCAT 1320
Db 1316 TGACCTGTTTCTCTGTCTGTGATGAATTCACAGCTTACATTAACAGCTGCTCAT 1375
QY 1321 TGGGAGCGCGCCAGGCTTAATCATAGCTGAGTACTGTTCTGGGAGAGAGTGTGC 1380
Db 1376 TGGGAGCGCGCCAGGCTTAATCATAGCTGAGTACTGTTCTGGGAGAGAGTGTGC 1435
QY 1381 TTCTCTTCATTCACATGTAAGTACCTGGATTAATTAATTCATTCATTCATTCATTC 1440
Db 1436 TTCTCTTCATTCACATGTAAGTACCTGGATTAATTAATTCATTCATTCATTCATTC 1495
QY 1441 TGGGAAATTTGGGATTCACCTCTCTTCTTCATGCTGTATGCTTCACTGCTGAGCTCT 1500
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QY 1501 ACCCAACCTGCTCAGAGACATGGGCTGGGGTGCATCCAGGCTCCAGAGTGGCA 1560
Db 1556 ACCCAACCTGCTCAGAGACATGGGCTGGGGTGCATCCAGGCTCCAGAGTGGCA 1615
QY 1561 GCATCATTTGCCCCCTACTTGTGTTTACCTGCTGTACCAAGAAATGCTGCCCTACATCG 1620
Db 1616 GCATCATTTGCCCCCTACTTGTGTTTACCTGCTGTACCAAGAAATGCTGCCCTACATCG 1675
QY 1621 TCATGGGTAGTCTGACTGCTGATTTGGAACTCAACCTTTTTCCTGAAAGTTGG 1680
Db 1676 TCATGGGTAGTCTGACTGCTGATTTGGAACTCAACCTTTTTCCTGAAAGTTGG 1735
QY 1681 GAATGACTTTCAGAAACCTTGAAGAGATGCAAGAAATGTAATGTTAGATCTGGGA 1740
Db 1736 GAATGACTTTCAGAAACCTTGAAGAGATGCAAGAAATGTAATGTTAGATCTGGGA 1795
QY 1741 AAAAAACAAGACATCAATGGAGAGAGAAAGAAATCCCAAGTTCTAATTAATGCTATTC 1800
Db 1796 AAAAAACAAGACATCAATGGAGAGAGAAAGAAATCCCAAGTTCTAATTAATGCTATTC 1855
QY 1801 GAAAAAATATACCCCATTTGGTGAAGTGAAGAAACAGAAAAATTAAGCCCTGGGAGAA 1860
Db 1856 GAAAAAATATACCCCATTTGGTGAAGTGAAGAAACAGAAAAATTAAGCCCTGGGAGAA 1915
QY 1861 ATTCGTTGTTCCACTGAATGAGACTGATTAACGATTAACCCAAATGAACCTTGTCT 1920
Db 1916 ATTCGTTGTTCCACTGAATGAGACTGATTAACGATTAACCCAAATGAACCTTGTCT 1975
QY 1921 ATCAAGAAATGCTGCTCATACAGTAATCTGAGATGATTCCTCCAGATATGCTTGTCT 1980
Db 1976 ATCAAGAAATGCTGCTCATACAGTAATCTGAGATGATTCCTCCAGATATGCTTGTCT 2035
QY 1981 TTACAACCAACCATTTCTAGAGAGTCTCTTACTCATTAATTAATGAAGATGGTGGT 2040
Db 2036 TTACAACCAACCATTTCTAGAGAGTCTCTTACTCATTAATTAATGAAGATGGTGGT 2095
QY 2041 AAGATGTTGAAAAACATGTTAGTCAAGAGCTGTAATAATACATATAAGATTAACACTC 2100
Db 2096 AAGATGTTGAAAAACATGTTAGTCAAGAGCTGTAATAATACATATAAGATTAACACTC 2155
QY 2101 ATTTCATTCATACAAATTAATCAATCAATTAATAAT 2135
Db 2156 ATTTCATTCATACAAATTAATCAATCAATTAATAAT 2190

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US-60-213-360-3396
; Sequence 3396, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preel
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; FILE REFERENCE: EX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; NUMBER OF SEQ ID NOS: 2000-06-21
; SOFTWARE: PERL program
; SEQ ID NO: 3396
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Inctyle ID No: 336027.6
US-60-213-360-3396

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Query Match 99.9%; Score 2131.8; DB 65; Length 2224;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCCCCGCTTGGCGCCCAATTTCTACACGCTGCTCTCCCGGGAGACTTTACATC 60
Db 56 CCCCCGCTTGGCGCCCAATTTCTACACGCTGCTCTCCCGGGAGACTTTACATC 115
QY 61 CTTGGGAGGCGCCACACTAAGACACTGCTCTGAGAAAGCTGTGATCACCCTGATTG 120
Db 116 CTTGGGAGGCGCCACACTAAGACACTGCTCTGAGAAAGCTGTGATCACCCTGATTG 175
QY 121 CAATTTTCGAGGCGGAGTGGGAGACATGCGGGAGCTACAGAGAGTATGCTTCTG 180
Db 176 CAATTTTCGAGGCGGAGTGGGAGACATGCGGGAGCTACAGAGAGTATGCTTCTG 235
QY 181 GCGAGTGGGCGCCCTTCACAGGCTCATCTTCTCCGCTCACGCGCAGCATATCCCA 240
Db 236 GCGAGTGGGCGCCCTTCACAGGCTCATCTTCTCCGCTCACGCGCAGCATATCCCA 295
QY 241 ATGGCTTCAATGTATGTAGTCAAGTGTCTCTGCGGGAGACCCCGGAGCAACCGCTGCGAG 300
Db 296 ATGGCTTCAATGTATGTAGTCAAGTGTCTCTGCGGGAGACCCCGGAGCAACCGCTGCGAG 355
QY 301 TGCCGAGCGCGGAGACCTGAGCAGCGCTGCGGCAACAACATGTCCTGCGGCTGC 360
Db 356 TGCCGAGCGCGGAGACCTGAGCAGCGCTGCGGCAACAACATGTCCTGCGGCTGC 415
QY 361 GGGAGGCGCGGAGTGCCTCCACAGCTGACAGCGCTACCGGCTCGCCACATGCGCACT 420
Db 416 GGGAGGCGCGGAGTGCCTCCACAGCTGACAGCGCTACCGGCTCGCCACATGCGCACT 475
QY 421 TCTCGCGCTCGGCGCTGAGCGCGGCGCGGCTGAGCTGCGGCGAGCTGGGCGAGTGGAGCAGAGA 480
Db 476 TCTCGCGCTCGGCGCTGAGCGCGGCGCGGCTGAGCTGCGGCGAGCTGGGCGAGTGGAGCAGAGA 535
QY 481 GCTGCTGATGAGCTGGGAGTTCAGCCAGAGAGTCTACTGTTCACCGTCTGACCGAGT 540
Db 536 GCTGCTGATGAGCTGGGAGTTCAGCCAGAGAGTCTACTGTTCACCGTCTGACCGAGT 595
QY 541 GGAATCTGAGTGTGAGAGCAACTGGAAGGTGCCCCCTACACAGCTGCCCTTCTGCTGAG 600
Db 596 GGAATCTGAGTGTGAGAGCAACTGGAAGGTGCCCCCTACACAGCTGCCCTTCTGCTGAG 655
QY 601 GCGTGTCTCTCGGCTCTTCTGTGTCTCGGCGAGCTGTACAGAGGTTTGGCAGGAAGAG 660
Db 656 GCGTGTCTCTCGGCTCTTCTGTGTCTCGGCGAGCTGTACAGAGGTTTGGCAGGAAGAG 715
QY 661 TTCTCTTCCAGACATGCGCTGTACAGACTGCGCTTACGCTTCTGACAGATTTTCTCATCA 720

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Db 716 TTCTCTGGCAACCTGGCTGACAGACTGGCTTCAGCTTCCTGAGATTTTCTTCATCA 775  
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 QY 781 TGGTACCTTCTACTAGAACAGAAATTTGGCAAGTCAGTTGATTAATTTCTCTA 840  
 Db 836 TGGTACCTTCTACTAGAACAGAAATTTGGCAAGTCAGTTGATTAATTTCTCTA 895  
 QY 841 CATTTAGAGTGTGCAATTTTGGATTTGGCTATATGCTGTGCACTGTTGTACT 900  
 Db 896 CATTTAGAGTGTGCAATTTTGGATTTGGCTATATGCTGTGCACTGTTGTACT 955  
 QY 901 TCATCAGAGACTGGCGAGTGTCTGTGCGCTGACGAGTGGCGAGTGTCTGTGCC 960  
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 QY 961 CGCTGTGTGTCTCAATTCCTGATCTCCCGATGGCTGATATCCAGAGAAATTTAG 1020  
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 QY 1021 AGGCTGAGATTCATCCAAAAAGCTGCAAAAAATGAACAACAGCTTACAGAGTGA 1080  
 Db 1076 AGGCTGAGATTCATCCAAAAAGCTGCAAAAAATGAACAACAGCTTACAGAGTGA 1135  
 QY 1081 TATTTGATTTCTGAGAGAGTAAATCCCTGAGACAGACAGAAAGCTTTCATTTGAG 1140  
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 Db 1256 CCTCAGTGGGTACTTGTGCTGCTGAGATGCTGCAATTTAATAGAGATGCTGCC 1315  
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 Db 1436 TTCTCTCATTCACATGAGTACCTGAGATTAATTTACTTTTATCCATTTGCTGCTG 1495  
 QY 1441 TGGGAAAAATTTGGATCACTCTGCTTCTCATGCTGATGTTCTCACTGCTGAGCTCT 1500  
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 Db 1556 ACCCAACCTGTCAGAGAAATGCGGTGGGGGTTCACATCCAGCGCTCCAGAGTGGCA 1615  
 QY 1561 GCATATTTGGCCCTTACTTTGTTTACTCGGTGCTTAACAAGATTTGCTGCTATCAG 1620  
 Db 1616 GCATATTTGGCCCTTACTTTGTTTACTCGGTGCTTAACAAGATTTGCTGCTATCAG 1675  
 QY 1621 TCATGGGTAGTCTGACTGTCTGATTTGAATCTTACCTTTTTCCTGAAATTTGG 1680  
 Db 1676 TCATGGGTAGTCTGACTGTCTGATTTGAATCTTACCTTTTTCCTGAAATTTGG 1735  
 QY 1681 GAATGACTTCCAGAAACCTTATAGAGAGATGCAAGAAATGTAATGTTAGATCTGGGA 1740  
 Db 1736 GAATGACTTCCAGAAACCTTATAGAGAGATGCAAGAAATGTAATGTTAGATCTGGGA 1795  
 QY 1741 AAAAAACAAGACTCAANTGAGAGACAGAAATCCCAAGGTCTTAATTAATGATCTCT 1800  
 Db 1796 AAAAAACAAGACTCAANTGAGAGACAGAAATCCCAAGGTCTTAATTAATGATCTCT 1855

QY 1801 GAAAAAATATCTACCCCATTTTGGTGAAGTGAAGAAAAACAGAAAAATAGACCTGTGAGAA 1860  
 Db 1856 GAAAAAATATCTACCCCATTTTGGTGAAGTGAAGAAAAACAGAAAAATAGACCTGTGAGAA 1915  
 QY 1861 ATTCGTTGTCCACGTAAATGACGTGACGTGAACGATGACACCAAAATGAACCTTGCT 1920  
 Db 1916 ATTCGTTGTCCACGTAAATGACGTGACGTGAACGATGACACCAAAATGAACCTTGCT 1975  
 QY 1921 ATCAAGAAATGCTGATACATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
 Db 1976 ATCAAGAAATGCTGATACATGATGATGATGATGATGATGATGATGATGATGATGAT 2035  
 QY 1981 TTCAAAACCAACATTTCTAGAGAGTCCCTTACTCTATTAATCAATGAATGATGATGAT 2040  
 Db 2036 TTCAAAACCAACATTTCTAGAGAGTCCCTTACTCTATTAATCAATGAATGATGATGAT 2095  
 QY 2041 AAGATGCTTGAAGAAATGTTAGTCAAGACGTGTAAATATATATTAAGATTAACACTC 2100  
 Db 2096 AAGATGCTTGAAGAAATGTTAGTCAAGACGTGTAAATATATATTAAGATTAACACTC 2155  
 QY 2101 ATTCCAAATCATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2135  
 Db 2156 ATTCCAAATCATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2190

RESULT 9  
 US-60-278-6685  
 ; Sequence 6685, Application US/60278258  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morris, Macdonald  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Diap, Diah  
 ; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using  
 ; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide  
 ; FILE REFERENCE: GX-0010-1 P  
 ; CURRENT APPLICATION NUMBER: US/60/278, 258  
 ; CURRENT FILING DATE: 2001-03-23  
 ; NUMBER OF SEQ ID NOS: 17730  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 6685  
 ; LENGTH: 2224  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc-feature  
 ; OTHER INFORMATION: Incyte ID No: 336027, 6  
 ; US-60-278-6685

Query Match 99.9%; Score 2131.8; DB 71; Length 2224;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCCGGTGGCGGCCCAATTTCTAACAGCCTGCTGTCCCGCGGAAACCTTCTAACATC 60  
 Db 56 CCCCCGGTGGCGGCCCAATTTCTAACAGCCTGCTGTCCCGCGGAAACCTTCTAACATC 115  
 QY 61 CTTGGGAGAGGCCCGACCTACAGACACTGCTCTGAGAAAGCTGTATCATCCCGTAGTTG 120  
 Db 116 CTTGGGAGAGGCCCGACCTACAGACACTGCTCTGAGAAAGCTGTATCATCCCGTAGTTG 175  
 QY 121 CAATTTCCGAGAGCGGAGTGGGAAGCATGGGGGACCTGACAGAGAGTATGCGCTCTGG 180  
 Db 176 CAATTTCCGAGAGCGGAGTGGGAAGCATGGGGGACCTGACAGAGAGTATGCGCTCTGG 235  
 QY 181 GCGAGTGGGGCCCTTCAGAGCCTCATCTTCTCTGCTCAAGCGCCAGCATCATCCCA 240  
 Db 236 GCGAGTGGGGCCCTTCAGAGCCTCATCTTCTCTGCTCAAGCGCCAGCATCATCCCA 295  
 QY 241 ATGCTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 Db 296 ATGCTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 355



301 TGGCGACGCGCGGAACCTGACAGAGCGCTGGGGCAACAACAGTGTGCCGCTGGCGCTGC  
QY  
356 TGGCGAGCGCGGGAACCTGAGAGCGCTGGGGCAACAACAGTGTGCCGCTGGCGCTGC  
Db  
361 GGGAGCGCGCGAGAGTGGCCACAGCTGACCGCTGACCGGCTGCGGCTACCTATGCGCACT  
QY  
416 GGGAGCGCGCGAGAGTGGCCACAGCTGACCGCTGACCGGCTGCGGCTACCTATGCGCACT  
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QY  
476 TCTCGGCGCGCTGGGGCTGGAGCGGGGCGGAGCTGAGACTGGGGGACGTGAGCAGAGA  
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QY  
596 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
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656 GCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
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836 TGGTAGCTTCACTACAGAGCAAGAACTTGGGCAAGTGTGCTATTAATCTGCA  
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1256 CCTGAGTGGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
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1261 TGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
QY  
1316 TGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
Db  
1321 TGGGAGCGCTGCGCGAGCGCTTATATCATAGCTGACAGTACTGTTCTGGGAGAGAGTGTG  
QY  
1376 TGGGAGCGCTGCGCGAGCGCTTATATCATAGCTGACAGTACTGTTCTGGGAGAGAGTGTG  
Db

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1501 ACCCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
QY  
1556 ACCCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
Db  
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QY  
1616 GCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
Db  
1621 TCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
QY  
1676 TCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
Db  
1681 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
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Db  
1741 AAAAACAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
QY  
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Db  
1801 GAAAAAATATCTACCCATTTGGTGAAGTGAAGAAACAGAAATTAAGACCTGTGAGAA  
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1856 GAAAAAATATCTACCCATTTGGTGAAGTGAAGAAACAGAAATTAAGACCTGTGAGAA  
Db  
1861 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
QY  
1916 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
Db  
1921 ATCAAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
QY  
1976 ATCAAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
Db  
1981 TTCAACAACCATTTTGAAGAGTGTCTTACTCATTAATTAATGAATGATGCT  
QY  
2036 TTCAACAACCATTTTGAAGAGTGTCTTACTCATTAATTAATGAATGATGCT  
Db  
2041 AAGATGCTTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
QY  
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Db  
2101 ATTCCAAATCATACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
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2156 ATTCCAAATCATACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
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RESULT 10  
US-60-324-185-10739  
; Sequence 10739, Application US/60324185  
; GENERAL INFORMATION:  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Lal, Preeti  
; APPLICANT: Diep, Dinh  
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING  
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE  
; FILE REFERENCE: GX-0019-1 P  
; CURRENT APPLICATION NUMBER: US/60/324,185  
; CURRENT FILING DATE: 2001-09-21  
; NUMBER OF SEQ ID NOS: 35862  
; SOFTWARE: PERL Program  
; SEQ ID NO 10739  
; LENGTH: 2224  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:



NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID No: 1398921.3  
US-60-324-185-10739

Query Match 99.9%; Score 2131.8; DB 76; Length 2224;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCCGCTTCGCGCCCAATTTCTACAGAGCTCCGTCGCCCGGGGAGAGTTCTATACATC 60  
DB 56 CCCCCGCTTCGCGCCCAATTTCTACAGAGCTCCGTCGCCCGGGGAGAGTTCTATACATC 115

QY 61 CTTGGGAGGCGCCCACTACAGACACTGCTCTGAGAAAGCTGTATCAGCCGTATGTTG 120  
DB 116 CTTGGGAGGCGCCCACTACAGACACTGCTCTGAGAAAGCTGTATCAGCCGTATGTTG 175

QY 121 CAAGTTTCGAGAGGCGAGTGGGAGAGATGCGGAGTACAGACAGAGTGTATGCTTCTGG 180  
DB 176 CAAGTTTCGAGAGGCGAGTGGGAGAGATGCGGAGTACAGACAGAGTGTATGCTTCTGG 235

QY 181 GCGAGTGGGCGCCCTTCAGAGCGCTCATCTTCTGCTGACAGCCAGATCATCCCA 240  
DB 236 GCGAGTGGGCGCCCTTCAGAGCGCTCATCTTCTGCTGACAGCCAGATCATCCCA 295

QY 241 ATGGCTTCAATGATATGTCAGTGTCTGCTGGGAGAACCCCGAGACCCGCTGTGAG 300  
DB 296 ATGGCTTCAATGATATGTCAGTGTCTGCTGGGAGAACCCCGAGACCCGCTGTGAG 355

QY 301 TGGCGAGACGCGCGAGACCTGAGAGCGCTGGGCGAACAAACATGTCCCGCTGCGCTGC 360  
DB 356 TGGCGAGACGCGCGAGACCTGAGAGCGCTGGGCGAACAAACATGTCCCGCTGCGCTGC 415

QY 361 GGGAGCGCGCGAGAGTGCACAGCTGACAGCGCTACCGGCTGCGGACACATCGCCACT 420  
DB 416 GGGAGCGCGCGAGAGTGCACAGCTGACAGCGCTACCGGCTGCGGACACATCGCCACT 475

QY 421 TCTCGGCGCTCGGCGCTGAGACCGGCGCGAGCTGAGACCTGGGAGACCTGAGACAGAGA 480  
DB 476 TCTCGGCGCTCGGCGCTGAGACCGGCGCGAGCTGAGACCTGGGAGACCTGAGACAGAGA 535

QY 481 GCTGCTGATGCTGGGAGTTCAGCGAGAGCTACCTGTCACACCGTCGTGACCGACT 540  
DB 536 GCTGCTGATGCTGGGAGTTCAGCGAGAGCTACCTGTCACACCGTCGTGACCGACT 595

QY 541 GGAATCTGTGTGTGAGAGCAACTGAGAAAGTGCCTTCACACACTCCCTGTTCTGTAG 600  
DB 596 GGAATCTGTGTGTGAGAGCAACTGAGAAAGTGCCTTCACACACTCCCTGTTCTGTAG 655

QY 601 GCGTGTCTCTCGGCTCTCTGCTGTCGCGGACGCTGTACAGACAGCTTGGCAGAGACAG 660  
DB 656 GCGTGTCTCTCGGCTCTCTGCTGTCGCGGACGCTGTACAGACAGCTTGGCAGAGACAG 715

QY 661 TTCTCTTCGCAACCATGGCTGTACAGACTGGCTTCAGCTTCGCAAGATTTCTCATCA 720  
DB 716 TTCTCTTCGCAACCATGGCTGTACAGACTGGCTTCAGCTTCGCAAGATTTCTCATCA 775

QY 721 GCTGGAGAGTGTCTACTGTGTATTTGTATCTGTGGAGTGGGCGCAGATCTCCCACTATG 780  
DB 776 GCTGGAGAGTGTCTACTGTGTATTTGTATCTGTGGAGTGGGCGCAGATCTCCCACTATG 835

QY 781 TGGTAGCCTTCATACAGAGAGAGAAATTTCTGGCAAGTCAAGTCTATATATTTCTCA 840  
DB 836 TGGTAGCCTTCATACAGAGAGAGAAATTTCTGGCAAGTCAAGTCTATATATTTCTCA 895

QY 841 CATTAGAGAGTGTACATTTTTCAGATTGGCTATATGCTGCTGCACTGTTTCTTACT 900  
DB 896 CATTAGAGAGTGTACATTTTTCAGATTGGCTATATGCTGCTGCACTGTTTCTTACT 955

QY 901 TCATCAGAGACTGGCGAGTGTCTGCTGCGCTGACGCTGCGGAGAGTGTCTGTCTTC 960  
DB 956 TCATCAGAGACTGGCGAGTGTCTGCTGCGCTGACGCTGCGGAGAGTGTCTGTCTTC 1015

QY 961 CGCTGTGTGTCTTCATTTCTGAAATCTCCCGATGGCTGATATCCAGAGAAAGATTAGAG 1020

DB 1016 CGCTGTGGGAGTTCACTTCCTGATCTCCCGCATGGCTGATATCCAGAGAAATTTAGAG 1075

QY 1021 AGGCTGAAGATATCTCCAAAAGCTGCAAAAATGACACACAGCTGTACAGACTGA 1080

DB 1076 AGGCTGAAGATATCTCCAAAAGCTGCAAAAATGACACACAGCTGTACAGACTGA 1135

QY 1081 TATTGATTCGTGGAGAGCTAAATCCCTGAAGCAGACAGAAAGCTTCAATTCGGACC 1140

DB 1136 TATTGATTCGTGGAGAGCTAAATCCCTGAAGCAGACAGAAAGCTTCAATTCGGACC 1195

QY 1141 TGTTCAGAGCTCGAATATTTGCAATATGACATATGCTCTTGTGCTATGATGCTGA 1200

DB 1196 TGTTCAGAGCTCGAATATTTGCAATATGACATATGCTCTTGTGCTATGATGCTGA 1255

QY 1201 CCTCAGTGGTACTTCTGCTGTCTGTGATGCTCTCAATTTACATGAGATGCTTACC 1260

DB 1256 CCTCAGTGGTACTTCTGCTGTCTGTGATGCTCTCAATTTACATGAGATGCTTACC 1315

QY 1261 TGAACGTTCCTCTCTGCTGATTTGAATTCACGTTTACATTAACAGCTGGCTGAT 1320

DB 1316 TGAACGTTCCTCTCTGCTGATTTGAATTCACGTTTACATTAACAGCTGGCTGAT 1375

QY 1321 TGGCAACGCTGCGGCGTTATATCATAGTGCAGTACTGTTGGGAGAGGCTGTC 1380

DB 1376 TGGCAACGCTGCGGCGTTATATCATAGTGCAGTACTGTTGGGAGAGGCTGTC 1435

QY 1381 TTTCTCTCATCACTGATGCTGCTGTGATTTATTTCTTATTCATTTGCTGTGCTATGC 1440

DB 1436 TTTCTCTCATCACTGATGCTGCTGTGATTTATTTCTTATTCATTTGCTGTGCTATGC 1495

QY 1441 TGGGAAAATTTGGGATCACTCTGCTCTCATGCTGTATGCTTCTCACTGAGCTCT 1500

DB 1496 TGGGAAAATTTGGGATCACTCTGCTCTCATGCTGTATGCTTCTCACTGAGCTCT 1555

QY 1501 ACCCAACCTGTGTCAGAAACATGCGGTGGGAGTCAATCAACGAGCTTCCAGAGTGGCA 1560

DB 1556 ACCCAACCTGTGTCAGAAACATGCGGTGGGAGTCAATCAACGAGCTTCCAGAGTGGCA 1615

QY 1561 GCATATGTCGCCCTACTGTTGTTACCTGCGGTCTTAACAGAAATGCTGCCATACATGC 1620

DB 1616 GCATATGTCGCCCTACTGTTGTTACCTGCGGTCTTAACAGAAATGCTGCCATACATGC 1675

QY 1621 TCATGGTAGTGTGCTGTCTGCTGATTTGAATCTTACACCTTTTCCCTGAAAGTTGG 1680

DB 1676 TCATGGTAGTGTGCTGTCTGCTGATTTGAATCTTACACCTTTTCCCTGAAAGTTGG 1735

QY 1681 GAATGACTTTCAGAAACCTTAGAGCAGATGACAGAAAGTGAATGTTTCAATCTGGGA 1740

DB 1736 GAATGACTTTCAGAAACCTTAGAGCAGATGACAGAAAGTGAATGTTTCAATCTGGGA 1795

QY 1741 AAAAAACAAGAGACTCAATGGAGACAGAAAGAAATCCCAAGTCTATTAATCTGATCTCT 1800

DB 1796 AAAAAACAAGAGACTCAATGGAGACAGAAAGAAATCCCAAGTCTATTAATCTGATCTCT 1855

QY 1801 GAAAAAATATCTACCCCATTTGCTGAAGTGAAGAAACAGAAATTAAGACCTGTGGAGA 1860

DB 1856 GAAAAAATATCTACCCCATTTGCTGAAGTGAAGAAACAGAAATTAAGACCTGTGGAGA 1915

QY 1861 ATTCTGTGTCCCATGAGAAATGAGTGTGATGATTTGACACCAAAATTAAGCTTGTCT 1920

DB 1916 ATTCTGTGTCCCATGAGAAATGAGTGTGATGATTTGACACCAAAATTAAGCTTGTCT 1975

QY 1921 ATCAGAAATGCTGCTCATACAGTAACTGTGATGATTTCTTCAGATTAATGCTTGTCT 1980

DB 1976 ATCAGAAATGCTGCTCATACAGTAACTGTGATGATTTCTTCAGATTAATGCTTGTCT 2035

QY 1981 TTACAACCAACCATTTCTAGAGAGTCTCTTACTCATTTAATCAATGAATGAATGGT 2040

DB 2036 TTACAACCAACCATTTCTAGAGAGTCTCTTACTCATTTAATCAATGAATGAATGGT 2095

QY 2041 AAGATGCTTGAAGAAACATGTTAGTACAGAGCTGTGAATATCATATAAGATTAACTC 2100

Db 2096 AAGATGCTTGAAGAACTGTTAGTCAAGACTGGTAAATATACATATATAAGATTAAACATC 2155  
QY 2101 ATTTCATCATATACAAATACTATATCAAAATAAAAT 2135  
Db 2156 ATTTCATCATATACAAATACTATATCAAAATAAAAT 2190

RESULT 11  
PCT-US02-17456-18  
: Sequence 18, Application PC/TUS0217456  
: GENERAL INFORMATION:  
: APPLICANT: EXELIXIS, INC.  
: TITLE OF INVENTION: SEC22AS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
: FILE REFERENCE: EX02-086C-PC  
: CURRENT APPLICATION NUMBER: PCT/US02/17456  
: PRIOR FILING DATE: 2002-06-03  
: PRIOR APPLICATION NUMBER: US 60/296,076  
: PRIOR FILING DATE: 2001-10-10  
: PRIOR APPLICATION NUMBER: US 60/328,605  
: PRIOR FILING DATE: 2001-06-05  
: PRIOR APPLICATION NUMBER: US 60/357,253  
: PRIOR FILING DATE: 2002-02-15  
: NUMBER OF SEQ ID NOS: 42  
: SOFTWARE: Patentin version 3.1  
: SEQ ID NO 18  
: LENGTH: 2135  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
PCT-US02-17456-18

Query Match 99.8%; Score 2130.2; DB 1; Length 2135;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2132; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCGGCTTGGCGCCCAATTTCTAACAGCCTGCTGCCCGGGAACGTTCTTAACATC 60  
Db 1 CCCCGGCTTGGCGCCCAATTTCTAACAGCCTGCTGCCCGGGAACGTTCTTAACATC 60  
QY 61 CTGGGGAGGCGCCCACTACAGACATCTCTGAGAAAGCTGTATCAACCGGTGTTG 120  
Db 61 CTGGGGAGGCGCCCACTACAGACATCTCTGAGAAAGCTGTATCAACCGGTGTTG 120  
QY 121 CAAGTTTCGAGAGGCGAGTGGGAAGCATGCGGAGTACAGAGAGTGTATGCTTCTG 180  
Db 121 CAAGTTTCGAGAGGCGAGTGGGAAGCATGCGGAGTACAGAGAGTGTATGCTTCTG 180  
QY 121 CAAGTTTCGAGAGGCGAGTGGGAAGCATGCGGAGTACAGAGAGTGTATGCTTCTG 180  
Db 121 CAAGTTTCGAGAGGCGAGTGGGAAGCATGCGGAGTACAGAGAGTGTATGCTTCTG 180  
QY 181 GCGAGTGGGCGCTTCCAGAGCCTCATCTTCTCTGCTCAAGCCAGCATATCCCA 240  
Db 181 GCGAGTGGGCGCTTCCAGAGCCTCATCTTCTCTGCTCAAGCCAGCATATCCCA 240  
QY 241 ATGACTTCATATGATATGATGATGCTGTCTTCTGCGGGGAGACCCGGAGACACCGCTG 300  
Db 241 ATGACTTCATATGATATGATGATGCTGTCTTCTGCGGGGAGACCCGGAGACACCGCTG 300  
QY 301 TGCAGGAGCGCGGAACTGAGAGCGCTGCGCAACAACAGATGTCGGCTGCGGCTGC 360  
Db 301 TGCAGGAGCGCGGAACTGAGAGCGCTGCGCAACAACAGATGTCGGCTGCGGCTGC 360  
QY 361 GGGAGGCGCGGAGTGGCCCAAGCTGAGCGCGCTACCGGCTGCGGCTGCGGCTG 420  
Db 361 GGGAGGCGCGGAGTGGCCCAAGCTGAGCGCGCTACCGGCTGCGGCTGCGGCTG 420  
QY 421 TCTCGGCGCTGCGGAGTGGAGCGCGGAGCTGAGACCTGAGGCGAGCTGAGAGCAGAGA 480  
Db 421 TCTCGGCGCTGCGGAGTGGAGCGCGGAGCTGAGACCTGAGGCGAGCTGAGAGCAGAGA 480  
QY 481 GCTGCGTGTGATGCTGGAGATTCAGCCAGAGAGCTACCGTGTCCACCGTGTACGAGAT 540  
Db 481 GCTGCGTGTGATGCTGGAGATTCAGCCAGAGAGCTACCGTGTCCACCGTGTACGAGAT 540  
QY 541 GGAATGCTGTGTGAGAGCACTGGAAGGTGCGCTTCCACCACTCCCTGTCTTCTGTAG 600  
Db 541 GGAATGCTGTGTGAGAGCACTGGAAGGTGCGCTTCCACCACTCCCTGTCTTCTGTAG 600

QY 601 GCGTGTCTCTCGGCTCTCTTCTGTCGCGGACACTGTACAGAGGTTTGGCAGGAAGACG 660  
Db 601 GCGTGTCTCTCGGCTCTCTTCTGTCGCGGACACTGTACAGAGGTTTGGCAGGAAGACG 660  
QY 661 TTCTCTTGGCAACCATGGCTGTACAGACTGGCTTACGCTTCCGTGACATTTTCTCATCA 720  
Db 661 TTCTCTTGGCAACCATGGCTGTACAGACTGGCTTACGCTTCCGTGACATTTTCTCATCA 720  
QY 721 GCTGGAGATGTTCACTGTGTTATTTGTCATCGTGGGATGGGACATGTCACATATG 780  
Db 721 GCTGGAGATGTTCACTGTGTTATTTGTCATCGTGGGATGGGACATGTCACATATG 780  
QY 781 TGGTAGCCTTCACTAGGAGACAGAAATTTTGGCAAGTCAGTTGATATATTTCTCTA 840  
Db 781 TGGTAGCCTTCACTAGGAGACAGAAATTTTGGCAAGTCAGTTGATATATTTCTCTA 840  
QY 841 CATTAGAGATGTCACATTTTGGAGTGGTATATGCTATGCTGCTGCTGCTGCTTACT 900  
Db 841 CATTAGAGATGTCACATTTTGGAGTGGTATATGCTATGCTGCTGCTGCTGCTTACT 900  
QY 901 TCATCAGAGACTGGCGGATGCTGCTGCGGCTGACGAGTGCAGGAGTGTGTGTC 960  
Db 901 TCATCAGAGACTGGCGGATGCTGCTGCGGCTGACGAGTGCAGGAGTGTGTGTC 960  
QY 961 CGCTGTGTGTTCACTTCTGATATCTCCCGATGCTATATCCAGAGAAATTTAG 1020  
Db 961 CGCTGTGTGTTCACTTCTGATATCTCCCGATGCTATATCCAGAGAAATTTAG 1020  
QY 1021 AGGCTGAGATATATCCAAAGCTGCAAAATTAACACATAGCTTACCAGACATGA 1080  
Db 1021 AGGCTGAGATATATCCAAAGCTGCAAAATTAACACATAGCTTACCAGACATGA 1080  
QY 1081 TATTGATTTCTGAGAGAGCTAAATCCCTGAAACAGACAAAGCTTTCATTCGAGC 1140  
Db 1081 TATTGATTTCTGAGAGAGCTAAATCCCTGAAACAGACAAAGCTTTCATTCGAGC 1140  
QY 1141 TGTGAGAGCTGGAATATGCAATAGACATATGCTTGTGTATGATAGTGA 1200  
Db 1141 TGTGAGAGCTGGAATATGCAATAGACATATGCTTGTGTATGATAGTGA 1200  
QY 1201 CCTCAGTGGTACTTGTCTGCTGATGCTCTTAATTTACATGAGATGCTTACC 1260  
Db 1201 CCTCAGTGGTACTTGTCTGCTGATGCTCTTAATTTACATGAGATGCTTACC 1260  
QY 1261 TGAATCTTCTCTCTGCTGCTGATTTCCAGCTTACATATACAGCTTGGCTGAT 1320  
Db 1261 TGAATCTTCTCTCTGCTGCTGATTTCCAGCTTACATATACAGCTTGGCTGAT 1320  
QY 1321 TGCAGAGCTGCCAGGCTTATATCATAGCTGAGTACTGTTGCGGAGAGAGTGTGC 1380  
Db 1321 TGCAGAGCTGCCAGGCTTATATCATAGCTGAGTACTGTTGCGGAGAGAGTGTGC 1380  
QY 1381 TTCTCTTATCACTAGTATCTGTGATATTTACTTCTATATGATGCTGTGATGC 1440  
Db 1381 TTCTCTTATCACTAGTATCTGTGATATTTACTTCTATATGATGCTGTGATGC 1440  
QY 1441 TGGGAAATTTGGATACCTGCTGCTTCTCAAGCTGTATGCTTCACTGCTAGGCT 1500  
Db 1441 TGGGAAATTTGGATACCTGCTGCTTCTCAAGCTGTATGCTTCACTGCTAGGCT 1500  
QY 1501 ACCCAACCTGCTGAGAAATGAGGCTGGGGGTCACATCCAGCGGCTCCAGAGTGGCA 1560  
Db 1501 ACCCAACCTGCTGAGAAATGAGGCTGGGGGTCACATCCAGCGGCTCCAGAGTGGCA 1560  
QY 1561 GCATCATTTGCCCTACTTTGTTACTCTGCTTACACAGAAATGCTGCCATATCG 1620  
Db 1561 GCATCATTTGCCCTACTTTGTTACTCTGCTTACACAGAAATGCTGCCATATCG 1620  
QY 1621 TCATGAGTATGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1680  
Db 1621 TCATGAGTATGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1680

QY	1681	GAATGACTCTCCAGAAACCTTTGAGCAGATGCGAAGATGAAATGGTTCAGATCTGGGA	1740
Db	1681	GAATGACTCTCCAGAAACCTTTGAGCAGATGCGAAGATGAAATGGTTCAGATCTGGGA	1740
QY	1741	AAAAACMAGAGACTCAATGAGCAGACAGACAAAATCCCAAGTTCCTATTAATCTGCATCTC	1800
Db	1741	AAAAACMAGAGACTCAATGAGCAGACAGACAAAATCCCAAGTTCCTATTAATCTGCATCTC	1800
QY	1801	GAATAAATATCTACCCCATTTGGTGAAGTGAATAACAGAAAATTAAGACCCCTGTGGAGAA	1860
Db	1801	GAATAAATATCTACCCCATTTGGTGAAGTGAATAACAGAAAATTAAGACCCCTGTGGAGAA	1860
QY	1861	ATTGCTGTCCCACTGAATGAGACTGACTGTAACGATGTGACACCAAAATGAACCTTGCT	1920
Db	1861	ATTGCTGTCCCACTGAATGAGACTGACTGTAACGATGTGACACCAAAATGAACCTTGCT	1920
QY	1921	ATCAGAGAAATGCTGTCATACAGCTAAACTCTGATGATTTCTTCAGATTAATGTCTTGCT	1980
Db	1921	ATCAGAGAAATGCTGTCATACAGCTAAACTCTGATGATTTCTTCAGATTAATGTCTTGCT	1980
QY	1981	TTTCAAAACCAACATTTCTAGAGAGTCCCTACTCATTAATTAAGAAATGGATGGT	2040
Db	1981	TTTCAAAACCAACATTTCTAGAGAGTCCCTACTCATTAATTAAGAAATGGATGGT	2040
QY	2041	AAGATGCTCTGAAACATGTTAGTCAAGAGACTGGTAAATATCATATTAAGATTAACACTC	2100
Db	2041	AAGATGCTCTGAAACATGTTAGTCAAGAGACTGGTAAATATCATATTAAGATTAACACTC	2100
QY	2101	ATTTCGAATCATACAAATACTATCTCCAAATATAAAAT	2135
Db	2101	ATTTCGAATCATACAAATACTATCTCCAAATATAAAAT	2135

RESULT 12  
PCT-US02-17456-16

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Sequence 16, Application PC/TUS0217456
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLIC22as AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-086C-PC
CURRENT APPLICATION NUMBER: PCT/US02/17456
CURRENT FILING DATE: 2002-06-03
PRIORITY APPLICATION NUMBER: US 60/296,076
PRIORITY FILING DATE: 2001-06-05
PRIORITY APPLICATION NUMBER: US 60/328,605
PRIORITY FILING DATE: 2001-10-10
PRIORITY APPLICATION NUMBER: US 60/357,253
PRIORITY FILING DATE: 2002-02-15
NUMBER OF SEQ. ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 2166
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-17456-16

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Query Match	99.8%;	Score 2130.2;	DB 1;	Length 2166;
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Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2132; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCCGCTCCGCCCAATTCTTACAGACCTGCGCTGTGCCCCGGGAACGTTTAACTC 60

Db 13 CCCCCGCTCCGCCCAATTCTTACAGACCTGTGCTGCCGCCGGGAACGTTTAACTC 72

QY 61 CTTGGGAGCGCCCGACGCTACAGACACTGTCTCTGAGAACGCTGTCACTACCCGTAAGTTG 120

Db 73 CTTGGGAGCGCCCGACGCTACAGACACTGTCTCTGAGAACGCTGTCACTACCCGTAAGTTG 132

QY 121 CAAAGTTTCGAGCGGCACTGGGAAAGCATCGCGGACTACGAGAGGTGTATCCGCTTCCTGG 180

Db 133 CAAAGTTTCGAGCGGCACTGGGAAAGCATCGCGGAGTACGAGAGGTGTATCCGCTTCCTGG 192

QY 181 GCGAGTGGGGGCCCTTCCAGCGCCTCATCTTCTTCCTGCTCAGCGCCAGCATCATCCCA 240

Db	193	GCAGATGGGGGCCCTTCCAGGCCCTCACTTCTTCTGCTAGGCGCCAGCATCCCCA	252
QY	241	ATGGCTTCATATGATATGTCAGTCTGTTTCCTGGCGGGAGCCCGAGAGCCGCTGAG	300
Db	253	ATGGCTTCATATGATATGTCAGTCTGTTTCCTGGCGGGAGCCCGAGAGCCGCTGAG	312
QY	301	TGCCGAGACGCCCGAACCCTGAGAGCGCTGGCGCAACAACATGTCCCGTGGCGTCC	360
Db	313	TGCCGAGACGCCCGAACCCTGAGAGCGCTGGCGCAACAACATGTCCCGTGGCGTCC	372
QY	361	GGGACGGCCGCGAGAGTGGCCCAAGTGTGACCGGTACCGGGTCCACATTCGCAACT	420
Db	373	GGGACGGCCGCGAGAGTGGCCCAAGTGTGACCGGTACCGGGTCCACATTCGCAACT	432
QY	421	TCTCGGCGCTCGGGGCTGAGACCGGGGCGGACGTGGAACCTGGGGGACGTGAGAGAGA	480
Db	433	TCTCGGCGCTCGGGGCTGAGACCGGGGCGGACGTGGAACCTGGGGGACGTGAGAGAGA	492
QY	481	GCTGCTCGATGGCTGGGAGTTCCAGCGAGACGTCTACTGTCCACGCTGTCGACCGAGT	540
Db	493	GCTGCTCGATGGCTGGGAGTTCCAGCGAGACGTCTACTGTCCACGCTGTCGACCGAGT	552
QY	541	GGATCTGGGTGTGAGGACAACCTGGAAAGTGGCCCTCACACGCTCCGTGTTCTGAG	600
Db	553	GGATCTGGGTGTGAGGACAACCTGGAAAGTGGCCCTCACACGCTCCGTGTTCTGAG	612
QY	601	GCGTGTCTCTCGGCTCCTTCTGTCGCGGACACTGTACAGACAGTTTGGCAGAAAGC	660
Db	613	GCGTGTCTCTCGGCTCCTTCTGTCGCGGACACTGTACAGAGGTTTGGCAGAAAGC	672
QY	661	TTCCTCTCGCAACCAATGCTGTACAGACTGCGCTTCAAGTTCTGTGACATTTTCTCATCA	720
Db	673	TTCCTCTCGCAACCAATGCTGTACAGACTGCGCTTCAAGTTCTGTGACATTTTCTCATCA	732
QY	721	GCTGGGAGATGTTCACTGTTATTTGTCATGTGGGCAATGGGCGACATTCGCAACATATG	780
Db	733	GCTGGGAGATGTTCACTGTTATTTGTCATGTGGGCAATGGGCGACATTCGCAACATATG	792
QY	781	TGATGAGCTTCATACTAGGAACAAGAAATCTTGGCAAGTCACTGTGATATATTTCTCTA	840
Db	793	TGATGAGCTTCATACTAGGAACAAGAAATCTTGGCAAGTCACTGTGATATATTTCTCTA	852
QY	841	CATTAGGAGTGTGCACATTTTTCGAGTTGGCTATATGCTGTGCCACTGTTTGGTTACT	900
Db	853	CATTAGGAGTGTGCACATTTTTCGAGTTGGCTATATGCTGTGCCACTGTTTGGTTACT	912
QY	901	TCAACAAGACGCGGAGTGTGCTGTGCGCTGACGCGTGGGAGGAGCGTGTGCC	960
Db	913	TCAACAAGACGCGGAGTGTGCTGTGCGCTGACGCGTGGGAGGAGCGTGTGTGCC	972
QY	961	CGCTGTGTGGTTCATTTCCGATTCGCCGAGTGGCTGATATCCGAGAGATTTAAG	1020
Db	973	CGCTGTGTGGTTCATTTCCGATTCGCCGAGTGGCTGATATCCGAGAGATTTAAG	1032
QY	1021	AGGCTGAAGATATATCCAAAAAGCTGCAAAAAATGAACAACACAGCTGTACACAGTGA	1080
Db	1033	AGGCTGAAGATATATCCAAAAAGCTGCAAAAAATGAACAACATCTGTACACAGTGA	1092
QY	1081	TATTTGATTTCTGTGAGAGACTTAATTCGCCCTGAAGAGACAGAAACCTTTTCATCTGAGC	1140
Db	1093	TATTTGATTTCTGTGAGAGACTTAATTCGCCCTGAAGAGACAGAAACCTTTTCATCTGAGC	1152
QY	1141	TGTTCCAGAGCTCGGAATATTTGCCATATGACCATTTGTCTTGGCTATGAGTGCAGA	1200
Db	1153	TGTTCCAGAGCTCGGAATATTTGCCATATGACCATTTGTCTTGGCTATGAGTGCAGA	1212
QY	1201	CCTCAGTGGGTACTTGTCTGTCTGTGATGTCTCAATTTACATGGAGATGCTTACC	1260
Db	1213	CCTCAGTGGGTACTTGTCTGTCTGTGATGTCTCAATTTACATGGAGATGCTTACC	1272
QY	1261	TGAACGTGTTCTCTCTGCTTATTTGAATTCAGCTTACATTTACAGCTGTGGCTGAT	1320

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Db 1273 TGAAGTCTTCTCTCTGCTGATTTGAAATTCACGATTAACAGCCTGGCTGCTAT 1332
QY 1321 TGGAAAGCTGCCAGGCGTTATATCATACGACGATGCTCTGGGAGAGGCTGCG 1380
Db 1333 TGGAAAGCTGCCAGGCGTTATATCATACGACGATGCTCTGGGAGAGGCTGCG 1392
QY 1381 TTCTCTTCAATCAATGCTACGCTGCTGCTTCTTCCATGCTGATGCTCTGCTGCTGCT 1440
Db 1393 TTCTCTTCAATCAATGCTACGCTGCTGCTGCTTCTTCCATGCTGCTGCTGCTGCTGCT 1452
QY 1441 TGGGAAATTTGGGATGACGCTGCTGCTTCTTCCATGCTGATGCTCTGCTGCTGCTGCT 1500
Db 1453 TGGGAAATTTGGGATGACGCTGCTGCTTCTTCCATGCTGATGCTCTGCTGCTGCTGCTGCT 1512
QY 1501 ACCCAACCCGTGTCAGGAACATGGCGGTGGGCTGATCCAGGCTCCAGAGTGGGA 1560
Db 1513 ACCCAACCCGTGTCAGGAACATGGCGGTGGGCTGATCCAGGCTCCAGAGTGGGA 1572
QY 1561 GCATCATTTGCCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1620
Db 1573 GCATCATTTGCCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1632
QY 1621 TCATGGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db 1633 TCATGGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1692
QY 1681 GAATGACTCTTCCAGAACTTATGAGACATGAGAAATGGAATGCTGCTGCTGCTGCTGCT 1740
Db 1693 GAATGACTCTTCCAGAACTTATGAGACATGAGAAATGGAATGCTGCTGCTGCTGCTGCT 1752
QY 1741 AAAAAACAGAGCTAATGAGAGACAGAAATCCCAAGTCTTCTTCTTCTTCTTCTTCTTCT 1800
Db 1753 AAAAAACAGAGCTAATGAGAGACAGAAATCCCAAGTCTTCTTCTTCTTCTTCTTCTTCT 1812
QY 1801 GAAAAATATCTACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Db 1813 GAAAAATATCTACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1872
QY 1861 ATTCGTTGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Db 1873 ATTCGTTGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1932
QY 1921 ATCAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1933 ATCAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1992
QY 1981 TTACAACCAACCATTTCTAGAGAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2040
Db 1993 TTACAACCAACCATTTCTAGAGAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2052
QY 2041 AAGATGCTCTTGAACATGTTAGTCAAGAGCTGTAATAATTAAGATTAAACACTC 2100
Db 2053 AAGATGCTCTTGAACATGTTAGTCAAGAGCTGTAATAATTAAGATTAAACACTC 2112
QY 2101 ATTCCATCATACAAATCTATCCAAATTAATAAT 2135
Db 2113 ATTCCATCATACAAATCTATCCAAATTAATAAT 2147

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; LENGTH: 2137
; TYPE: DNA
; ORGANISM: HUMAN
; US-60-258-275-536

Query Match
Best local similarity 99.8%; Pred. No. 0;
Matches 2132; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 CCCGCGCTTCGCGCCCAATTTCTAACAGCTGCTGCTCCCGGGAACGTTCTTAACATC 60
Db 2 CCCGCGCTTCGCGCCCAATTTCTAACAGCTGCTGCTGCTCCCGGGAACGTTCTTAACATC 61
QY 61 CTTGGGAGCGCCCGAGTACAGACATGCTGCTGAGAACCTGTCAACACCTTACTG 120
Db 62 CTTGGGAGCGCCCGAGTACAGACATGCTGCTGAGAACCTGTCAACACCTTACTG 121
QY 121 CAAGTTTGGAGCGGAGTGGGAAAGCATGCGGAGCATGAGAGAGTGTGCTGCTG 180
Db 122 CAAGTTTGGAGCGGAGTGGGAAAGCATGCGGAGCATGAGAGAGTGTGCTGCTG 181
QY 181 GCGAGTGGGCGCTTCCAGGCTCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 182 GCGAGTGGGCGCTTCCAGGCTCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
QY 241 ATGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 242 ATGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
QY 301 TCCGAGCGCGCGAACCCTGAGACAGCGGCTGCGCAACACATGCTGCTGCTGCTGCTGCTGCT 360
Db 302 TCCGAGCGCGCGAACCCTGAGACAGCGGCTGCGCAACACATGCTGCTGCTGCTGCTGCTGCT 361
QY 361 GGGAGCGCGCGAGTGGCGCCACAGCTGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 362 GGGAGCGCGCGAGTGGCGCCACAGCTGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
QY 421 TCTGCGGCTGCGGCTGAGCGCGGCGCGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 480
Db 422 TCTGCGGCTGCGGCTGAGCGCGGCGCGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 481
QY 481 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 482 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
QY 541 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 542 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
QY 601 GCGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
Db 602 GCGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
QY 660 GTTCTCTTCCGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
Db 662 GTTCTCTTCCGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
QY 720 AGCTGGAGAGTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
Db 722 AGCTGGAGAGTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
QY 780 GTGCTACCTTCACTAGAGAACAGAAATCTTGGCAAGTCACTGCTGCTGCTGCTGCTGCTGCT 839
Db 782 GTGCTACCTTCACTAGAGAACAGAAATCTTGGCAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCT 841
QY 840 ACATTAGAGAGTGGCAATTTTGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
Db 842 ACATTAGAGAGTGGCAATTTTGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 901
QY 900 TTCAATCAGAGTGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
Db 902 TTCAATCAGAGTGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961

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RESULT 13
US-60-258-275-536
; Sequence 536, Application US/60258275
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: C1001026-PROV
; CURRENT APPLICATION NUMBER: US/60/258,275
; NUMBER OF SEQ ID NOS: 717
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 536

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Db	541	CTGTACAGCATGCGCTTACAGCTTCCGTGCAGATTTTCTCCATCAGCTGGGAGATGTTCACTG	600
QY	739	TGTTATTATTTGTCATCGTGGGCATAGGGCCAGATCTCCAACTATGTGGTAGCCCTTCATACTAG	798
Db	601	TGTTATTATTTGTCATCGTGGGCATAGGGCCAGATCTCCAACTATGTGGTAGCCCTTCATACTAG	660
QY	739	GAAACAGAAATTTCTTGSCAAGTAGTCAGTTCGATTAATATTTCTTCATATAGGAGTGCACAT	858
Db	661	GAAACAGAAATTTCTTGSCAAGTAGTCAGTTCGATTAATATTTCTTCATATAGGAGTGCACAT	720
QY	839	TTTTTGCAGTTGGCTATATGCTGTCGCCACTGTTTTGCTTACTTCATCAGAGACTGGCGGA	918
Db	721	TTTTTGCAGTTGGCTATATGCTGTCGCCACTGTTTTGCTTACTTCATCAGAGACTGGCGGA	780
QY	919	TGCTCTCGTGGCGGTGAGCGGTGGGGAGATCGTGTGTCCCGCTGTGTGTGCTTATTC	978
Db	781	TGCTCTCGTGGCGGTGAGCGGTGGGGAGATCGTGTGTCCCGCTGTGTGTGCTTATTC	840
QY	979	CTGAATCTCCCGATGGCTGATATCCACAGAGAAAGATTATAGAGAGCTGAAGATATATCC	1033
Db	841	CTGAATCTCCCGATGGCTGATATCCACAGAGAAAGATTATAGAGAGCTGAAGATATATCC	900
QY	1039	AAAAAGCTGCAAAAATTGAACAACACAGCTGTACCAAGCTGATATTGATTTCTGTGGAGG	1099
Db	901	AAAAAGCTGCAAAAATTGAACAACACAGCTGTACCAAGCTGATATTGATTTCTGTGGAGG	960
QY	1099	AGCTAAATCCCTGTGAAGCAGCAGAAAGCTTTCATCTGTGACCTGTTCAGAGCTCGGAATA	1158
Db	961	AGCTAAATCCCTGTGAAGCAGCAGAAAGCTTTCATCTGTGACCTGTTCAGAGCTCGGAATA	1022
QY	1159	TTGGCATATATGACCTTATATGCTTTGTGTGCTATGTGATCGTACCTGAGTGGGTACTTGG	1218
Db	1021	TTGGCATATATGACCTTATATGCTTTGTGTGCTATGTGATCGTACCTGAGTGGGTACTTGG	1080
QY	1219	CTGTGCTCTGTGGATCTCTTAATTACATGGAGATCGCTTACTCGAAGCTGTTTCCATCTGTG	1278
Db	1081	CTGTGCTCTGTGGATCTCTTAATTACATGGAGATCGCTTACTCGAAGCTGTTTCCATCTGTG	1144
QY	1279	CCTTGATTTGAATTTCCAGCTTACATTTACAGCCGTGGCTGTATTTGGAAAGCTGCCAGGC	1338
Db	1141	CCTTGATTTGAATTTCCAGCTTACATTTACAGCCGTGGCTGTATTTGGAAAGCTGCCAGGC	1200
QY	1339	GTATATCATATAGCTCAGTACTAGTGTCTGGGGAGGAGGTGCTTCTTCATATTCACATGG	1398
Db	1201	GTATATCATATAGCTCAGTACTAGTGTCTGGGGAGGAGGTGCTTCTTCATATTCACATGG	1266
QY	1399	TACCTGTGGAATTAATCTTCTTATTCAGATTTGCTGTGTCATCTGTGGAAAAATTTGGAGTCA	1458
Db	1261	TACCTGTGGAATTAATCTTCTTATTCAGATTTGCTGTGTCATCTGTGGAAAAATTTGGAGTCA	1322
QY	1459	CCCTGCGCTTTCACATGCTGTATATGCTTCACATGCTGAGCTTACCCAACTCGTGTGACAGA	1518
Db	1321	CCCTGCGCTTTCACATGCTGTATATGCTTCACATGCTGAGCTTACCCAACTCGTGTGACAGA	1380
QY	1519	ACATGGCGGTGGGGGTACATCCACAGGGCTCCAGAGTGGGAGCATCTTCCCCCTACT	1578
Db	1381	ACATGGCGGTGGGGGTACATCCACAGGGCTCCAGAGTGGGAGCATCTTCCCCCTACT	1440
QY	1579	TTGTATTACTGTGGGTCTTACACAGAAATGCTGCCCTACATCTGATAGGGTATGCTGACTG	1638
Db	1441	TTGTATTACTGTGGGTCTTACACAGAAATGCTGCCCTACATCTGATAGGGTATGCTGACTG	1500
QY	1639	TTCGATTTGGAAATCTCACCCCTTTTTTCCCTGAAAGTTTGGGAATGACCTTCCAGAAA	1698
Db	1501	TTCGATTTGGAAATCTCACCCCTTTTTTCCCTGAAAGTTTGGGAATGACCTTCCAGAAA	1560
QY	1699	CCTTAGAGCAGATGCAGAAAGTGAATGGTTACAGATCTGGGAAAAAACAAGACACTCAA	1758
Db	1561	CCTTAGAGCAGATGCAGAAAGTGAATGGTTACAGATCTGGGAAAAAACAAGACACTCAA	1620
QY	1759	TGGAGACAGAAAGAAATCCCAAGGTCTCTAATTAATGCTATTTCTGAAAAAATATCTACCCCA	1818
Db	1621	TGGAGACAGAAAGAAATCCCAAGGTCTCTAATTAATGCTATTTCTGAAAAAATATCTACCCCA	1680

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Oy      1819 TTTGGTGAAGGAAAAACAGAAAAATAGACCCTGTGAGAAATTCGTTGCCA 1874
Db      1681 TTTGGTGAAGTGAACAAACAGAAATAAGACCCTGTGAGAAATTCGTTGCCA 1736

RESULT 15
: Sequence 1990, Application US/60226176
: GENERAL INFORMATION:
: APPLICANT: Ring, Huijun Z.
: APPLICANT: Malsen, Gareth
: APPLICANT: Townley, David
: APPLICANT: Morris, MacDonald
: TITLE OF INVENTION: Single Nucleotide Polymorphisms associated with ADME Genes
: FILE REFERENCE: GA-0013-1 P
: CURRENT APPLICATION NUMBER: US/60/226,176
: CURRENT FILING DATE: 2000-08-16
: NUMBER OF SEQ ID NOS: 2447
: SOFTWARE: PERL Program
: SEQ ID NO 1990
: LENGTH: 1656
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: GB:AB007448.1
: US-60-226-176-1990

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Query Match	77.6%	Score 1656;	DB 66;	Length 1656;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1656;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	14	ATGCGGAGCTACGACGAGGATGATTCGCTTCGCGGCGAGTGGGGGCGCTTCACAGCGCTC	20
Db	1	ATTCGGGACTACGACGAGGATGATTCGCTTCGCGGCGAGTGGGGGCGCTTCACAGCGCTC	60
QY	207	ATCTCTTCCTGCTGCAGCGCCAGACATCATCCCCAAATGGCTTC AATGATATGCTAGTCGTG	266
Db	61	ATCTCTTCCTGCTGCAGCGCCAGACATCATCCCCAAATGGCTTC AATGATATGCTAGTCGTG	126
QY	267	TTCCTGGCGGGGACCCCCGAGACCGGCTGTGCAATGGCGGACGCCGGACACTGACAGC	326
Db	121	TTCCTGGCGGGGACCCCCGAGACCGGCTGTGCAATGGCGGACGCCGGACACTGACAGC	186
QY	327	GCTGGCGGCAACAAAGTGTCCCGGCTGGGGGCTGGGGAAACGGCGGGAGGTGCCCCAACG	386
Db	181	GCTGGCGGCAACAAAGTGTCCCGGCTGGGGGCTGGGGAAACGGCGGGAGGTGCCCCAACG	246
QY	387	TGCAGCGGCTACCGGCTGCGCACCATTCGCGCACTTCTCGGGCTCTCGGGCTGGAGCCGGG	446
Db	241	TGCAGCGGCTACCGGCTGCGCACCATTCGCGCACTTCTCGGGGCTCTCGGGCTGGAGCCGGG	306
QY	447	CGGACAGTGGAGCTGGGGGACGCTGGAGCAGGAGAGCTCCTGTGATGGCTGGAGTTACG	506
Db	301	CGGACAGTGGAGCTGGGGGACGCTGGAGCAGGAGAGCTCCTGTGATGGCTGGAGTTACG	366
QY	507	CAGAGCTGTACCTGTGCCACCGTCCGAGCCGAGGTGGATTCGTGTGGAGAGAACATGG	566
Db	361	CAGAGCTGTACCTGTGCCACCGTCCGAGCCGAGGTGGATTCGTGTGGAGAGAACATGG	426
QY	567	AAGGTGCCCCCTACGACACTCCCTGTTCTTCGTGAGCGTGCCTCTCGGCTCCTTGCTGC	626
Db	421	AAGGTGCCCCCTACGACACTCCCTGTTCTTCGTGAGCGTGCCTCTCGGCTCCTTGCTGC	486
QY	627	GGGACAGCTGCAGACAGGTTTGGCAGAGAAAGCTTCTTTCGACACCATAGCTGTACAG	686
Db	481	GGGACAGCTGCAGACAGGTTTGGCAGAGAAAGCTTCTTTCGACACCATAGCTGTACAG	546
QY	687	ACGAGGTTACGTTCTCTGAGATTTCCTCCATCCAGAGCTGGGAGATGTTCACTGCTATTTT	746
Db	541	ACGAGGTTACGTTCTCTGAGATTTCCTCCATCCAGAGCTGGGAGATGTTCACTGCTATTTT	606

Search completed: July 5, 2003, 08:28:14  
Job time : 4831 secs

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QY 747 GTCATGCGGGGATGGGCGGAGATCTCCAACTATGTGGTAGCCCTCATCTAGAACAGAA 806
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Db 601 GTCATGCGGGGATGGGCGGAGATCTCCAACTATGTGGTAGCCCTCATCTAGAACAGAA 660
QY 807 ATTCTGGCAAGTCATTTGTTATATTTCTTACTATTAGAGTGTGACATTTTGTGCA 866
    |||||||
Db 661 ATTCTGGCAAGTCATTTGTTATATTTCTTACTATTAGAGTGTGACATTTTGTGCA 720
QY 867 GTTGGCTATATGCTGTGCTGCTGTTGCTTACTTCTATCAGAGACTGGGGATGCTGCG 926
    |||||||
Db 721 GTTGGCTATATGCTGTGCTGCTGTTGCTTACTTCTATCAGAGACTGGGGATGCTGCG 780
QY 927 CTGGCGCTACGGGTGCGGGAGTGTGTGTCCGCTGTGGTGTTCATTCTGTAATCT 986
    |||||||
Db 781 CTGGCGCTACGGGTGCGGGAGTGTGTGTCCGCTGTGGTGTTCATTCTGTAATCT 840
QY 987 CCCCCGATGGCTGATATCCAGAGAAATTTAGAGAGCTGAAGATATCATCCAAAAGCT 1046
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Db 841 CCCCCGATGGCTGATATCCAGAGAAATTTAGAGAGCTGAAGATATCATCCAAAAGCT 900
QY 1047 GCAAAATGAAACACACAGCTGTACAGAGATGATATTGATTCTGTGGAGAGCTAAAT 1106
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Db 901 GCAAAATGAAACACACAGCTGTACAGAGATGATATTGATTCTGTGGAGAGCTAAAT 960
QY 1107 CCCCAGAACAGCAGAAAGCTTTCATTCTGACCTGTTCAGAGCTCGAATATTGCCATA 1166
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Db 961 CCCCAGAACAGCAGAAAGCTTTCATTCTGACCTGTTCAGAGCTCGAATATTGCCATA 1020
QY 1167 ATGACCATATGCTTGTGCTATGAGATGCTGACCTCAGTGGGTTACTTGTCTGTCT 1226
    |||||||
Db 1021 ATGACCATATGCTTGTGCTATGAGATGCTGACCTCAGTGGGTTACTTGTCTGTCT 1080
QY 1227 CTGATGCTCTAAATTTACATGAGATGCTTACCTGACTGTTCTCTGCTGCTGANT 1286
    |||||||
Db 1081 CTGATGCTCTAAATTTACATGAGATGCTTACCTGACTGTTCTCTGCTGCTGANT 1140
QY 1287 GAAATTCAGCTTACATTACAGCTGTGCTATTGCGAACCTGCCAGGCGTTATATC 1346
    |||||||
Db 1141 GAAATTCAGCTTACATTACAGCTGTGCTATTGCGAACCTGCCAGGCGTTATATC 1200
QY 1347 ATAGCGCAGTACTGTTCTGGGGAGAGGTGCTTCTTCTATCAACTGTAACCTGTG 1406
    |||||||
Db 1201 ATAGCGCAGTACTGTTCTGGGGAGAGGTGCTTCTTCTATCAACTGTAACCTGTG 1260
QY 1407 GATTATTACTTCTTATCCATTGCTGTGCTATGCTGGAATAATTGGATCACTGTGCT 1466
    |||||||
Db 1261 GATTATTACTTCTTATCCATTGCTGTGCTATGCTGGAATAATTGGATCACTGTGCT 1320
QY 1467 TTCTCAGTCTATATGCTTCTCACTGCTGAGCTCTAACCAACCTGTGAGAACTGGCG 1526
    |||||||
Db 1321 TTCTCAGTCTATATGCTTCTCACTGCTGAGCTCTAACCAACCTGTGAGAACTGGCG 1380
QY 1527 GTGGGGGTACATCCACGGCTCCAGAGTGGGAGCATCATGCCCCCTACTTGTGTAC 1586
    |||||||
Db 1381 GTGGGGGTACATCCACGGCTCCAGAGTGGGAGCATCATGCCCCCTACTTGTGTAC 1440
QY 1587 CTGGGTGCTTACACAGAAATGCTGCCCTACATCGTCAATGGGTAGTCTGACTGCTGANT 1646
    |||||||
Db 1441 CTGGGTGCTTACACAGAAATGCTGCCCTACATCGTCAATGGGTAGTCTGACTGCTGANT 1500
QY 1647 GGAATCTTACCCCTTTTTCCTGAAAGTTGGGAATGACTTTCAGAAAACCTTAGAG 1706
    |||||||
Db 1501 GGAATCTTACCCCTTTTTCCTGAAAGTTGGGAATGACTTTCAGAAAACCTTAGAG 1560
QY 1707 CAGATGCAAGAAAGTGAATGTTGATGATCTGGGAAAAAACAAGAGACTCAATGAGACA 1766
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Db 1561 CAGATGCAAGAAAGTGAATGTTGATGATCTGGGAAAAAACAAGAGACTCAATGAGACA 1620
QY 1767 GAAGAAATCCCAAGTTCTAATAACTCATTTCTGA 1802
    |||||||
Db 1621 GAAGAAATCCCAAGTTCTAATAACTCATTTCTGA 1656
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 07:02:38 ; Search time 1582 Seconds  
(without alignments)  
9657.709 Million cell updates/sec

Title: US-09-521-195B-2

Perfect score: 2135  
Sequence: 1 cccgcgttcgcgcgcacat.....atactatccaataaataat 2135

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8255821 seqs, 3578102051 residues

Total number of hits satisfying chosen parameters: 16511642

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

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19: /cgn2\_6/ptodata/2/pna/US60\_NEW.COMB.seq3:\*  
20: /cgn2\_6/ptodata/2/pna/US60\_NEW.COMB.seq4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2130.2	99.8	2135	US-10-170-235-41510	Sequence 41510, A
2	2130.2	99.8	2214	US-10-327-189-1	Sequence 37, Appl1
3	2103.4	98.5	2136	US-10-327-189-37	Sequence 37, Appl1
4	1940.4	90.9	2343	US-09-724-676-48345	Sequence 48345, A
5	1940.4	90.9	2343	US-09-724-676-48345	Sequence 48345, A
6	1310.6	61.4	2080	US-10-144-771-9909	Sequence 9909, Ap
7	1065.8	48.9	3252	US-09-949-016-438	Sequence 438, App
8	1064.2	48.8	3252	US-10-327-189-3	Sequence 3, Appl1
9	1023	47.9	3223	US-09-949-016-2058	Sequence 2058, Ap
10	1016.2	47.6	3223	US-10-170-235-41508	Sequence 41508, A
11	1016.2	47.6	3223	US-60-453-135-4827	Sequence 4827, Ap
12	1016.2	47.6	3223	US-60-453-050-4827	Sequence 4827, Ap
13	1016.2	47.6	3223	US-60-456-412-4827	Sequence 4827, Ap

14	994	46.6	2574	14	US-10-144-771-9977	Sequence 9977, Ap
15	982.8	46.0	3037	2	PCT-US03-03482-3472	Sequence 3472, Ap
16	982.8	46.0	3037	2	PCT-US03-03194-3384	Sequence 3384, Ap
17	982.8	46.0	3037	14	US-10-301-856-969	Sequence 969, App
18	982.8	46.0	3037	15	US-10-357-507-3472	Sequence 3472, Ap
19	982.8	46.0	3037	18	US-60-436-643-3384	Sequence 3384, Ap
20	905.6	42.4	2297	14	US-10-144-771-9906	Sequence 9906, Ap
21	905.6	42.4	2297	15	US-10-326-820-1	Sequence 1, Appl1
22	539	25.2	692	15	US-10-170-235-34118	Sequence 34118, A
23	539	25.2	11285	15	US-60-466-412-85914	Sequence 85914, A
24	526.4	24.7	54550	15	US-10-327-189-42	Sequence 42, Appl1
25	393	18.4	393	15	US-10-170-235-27867	Sequence 27867, A
26	364.8	17.1	29871	11	US-09-949-016-12180	Sequence 12180, A
27	364.8	17.1	29876	11	US-09-949-016-13800	Sequence 13800, A
28	364	17.0	37876	19	US-60-466-412-85911	Sequence 85911, A
29	360.2	16.9	614	15	US-10-327-189-8	Sequence 8, Appl1
30	360.2	16.9	26850	15	US-10-327-189-41	Sequence 41, Appl1
31	247.6	11.6	475	2	PCT-US03-13853-2908	Sequence 2908, Ap
32	195.6	9.2	2152	14	US-10-152-319A-1921	Sequence 1921, Ap
33	195.6	9.2	2152	14	US-10-301-856-1080	Sequence 1080, Ap
34	194.8	9.1	2480	18	US-60-453-135-6288	Sequence 6288, Ap
35	194.8	9.1	2480	18	US-60-453-050-6288	Sequence 6288, Ap
36	194.8	9.1	2480	19	US-60-466-412-6288	Sequence 6288, Ap
37	193.6	9.1	1725	2	PCT-US02-19592-27	Sequence 27, Appl1
38	193.6	9.1	2257	2	PCT-US02-29560-58	Sequence 58, Appl1
39	193.6	9.1	2257	2	PCT-US02-19592-26	Sequence 26, Appl1
40	193.6	9.1	2257	14	US-10-245-882-58	Sequence 58, Appl1
41	193.6	9.1	2257	16	US-10-295-027-299	Sequence 299, App
42	193.6	9.1	2480	15	US-10-170-235-22149	Sequence 22149, A
43	193	9.0	2138	14	US-10-144-771-7194	Sequence 7194, Ap
44	188.2	8.8	2403	10	US-09-724-676-47336	Sequence 47336, A
45	188.2	8.8	2403	10	US-09-724-676-47336	Sequence 47336, A

## ALIGNMENTS

RESULT 1  
US-10-170-235-41510  
; Sequence 41510, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU  
; FILE REFERENCE: C1001380  
; CURRENT APPLICATION NUMBER: US/10/170, 235  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 42514  
; SEQ ID NO 41510  
; LENGTH: 2135  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-41510

Query Match 99.8%; Score 2130.2; DB 15; Length 2135;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2132; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	CCCCGGCTTGGCGCCCAATTTCTTACAGCCTGCTGCTCCCGGGAGAGCTTACATC 60	
DB	1	CCCCGGCTTGGCGCCCAATTTCTTACAGCCTGCTGCTCCCGGGAGAGCTTACATC 60	
QY	61	CTTGGGAGGAGCCCGACCTACAGACCTCTCGAGAGCGTGCATACCGGTAGTTC 120	
DB	61	CTTGGGAGGAGCCCGACCTACAGACCTCTCGAGAGCGTGCATACCGGTAGTTC 120	
QY	121	CAAGTTTCGAGGCGGAGTGGAGAGCATGCGGAGCTACGAGAGTATCGCTTCTGG 180	
DB	121	CAAGTTTCGAGGCGGAGTGGAGAGCATGCGGAGCTACGAGAGTATCGCTTCTGG 180	
QY	181	CGAGTGGGAGGCGCTTCCAGCGCTATCTTCTTCTGCTACGCGCAGATCATTC 240	
DB	181	CGAGTGGGAGGCGCTTCCAGCGCTATCTTCTTCTGCTACGCGCAGATCATTC 240	

QY	241	ATGGCTTCAAGATGATGTGACATGCTGTTTCCGTGGGGGGAGACCCCGGAGACCGCGTGTGAG	300
Db	241	ATGGCTTCAAGATGATGTGATGTGATGTGATGTCTGTTCCTGGGGGGAGACCCCGGAGACCGCGTGTGAG	300
QY	301	TGCCGGAGCGCCGCAACCTGTAGACAGCGCGCTGGGCCCAACACATGATGTCCCGTGGGGCTGC	360
Db	301	TGCCGGAGCGCCGCAACCTGTAGACAGCGCGCTGGGCCCAACACATGATGTCCCGTGGGGCTGC	360
QY	361	GGGACGGCCGGAGAGTGTCCCAACAGCTGACGCCGTACCCGGCTGGCCACCATGGCCAACT	420
Db	361	GGGACGGCCGGAGAGTGTCCCAACAGCTGACGCCGTACCCGGCTGGCCACCATGGCCAACT	420
QY	421	TCTGGGCGCTGGGGCTGGAGCGGGGGCGCAGCTGGAGCTGGGGCAGCTGGAGCAGAGA	480
Db	421	TCTGGGCGCTGGGGCTGGAGCGGGGGCGCAGCTGGAGCTGGGGCAGCTGGAGCAGAGA	480
QY	481	GCTGCTCGTAGATGCTGGAGTTTCAGCCAGAGCGTCTACCTGTGTCCACCGTGTGACCGAGT	540
Db	481	GCTGCTCGTAGATGCTGGAGTTTCAGCCAGAGCGTCTACCTGTGTCCACCGTGTGACCGAGT	540
QY	541	GGAAATCTGGTGTGGAGGACAACTGGAAAGGGCCCTACCAACCTCCCTGTTCCTGTAG	600
Db	541	GGAAATCTGGTGTGGAGGACAACTGGAAAGGGCCCTACCAACCTCCCTGTTCCTGTAG	600
QY	601	GCGTGTCTCTGGGCTCTTCTGTCGCCGGGCGAGCTGTACAGACAGGTTTTGGCAGGAAGACG	660
Db	601	GCGTGTCTCTGGGCTCTTCTGTCGCCGGGCGAGCTGTACAGACAGGTTTTGGCAGGAAGACG	660
QY	661	TTCTCTTTCGCACCAATGGCTGTACAGACTGGCGTTACAGTCTCTGTGCAGATTTTCTTCATCA	720
Db	661	TTCTCTTTCGCACCAATGGCTGTACAGACTGGCGTTACAGTCTCTGTGCAGATTTTCTTCATCA	720
QY	721	GCTGGGAGATTTTCACTGTGTATTGTTCATCTGCGGAGTGGGCATGGGCATCTCCAACTTG	780
Db	721	GCTGGGAGATTTTCACTGTGTATTGTTCATCTGCGGAGTGGGCATGGGCATCTCCAACTTG	780
QY	781	TGTGAGCCTTCATCTAGAGAAACAGAAATTTCTTGGCAAGTCAATTGTATTATTTCTCTA	840
Db	781	TGTGAGCCTTCATCTAGAGAAACAGAAATTTCTTGGCAAGTCAATTGTATTATTTCTCTA	840
QY	841	CATTAGGAGTGTGCACATTTTTTTCAGTGTGGCTTATGCTGCTGCACATGTATTGGTACT	900
Db	841	CATTAGGAGTGTGCACATTTTTTTCAGTGTGGCTTATGCTGCTGCACATGTATTGGTACT	900
QY	901	TCATCAGAGACTGGCGGATGCTGCTGTGCGCTGACAGGTCCGGGATGCTGTGTCTCC	960
Db	901	TCATCAGAGACTGGCGGATGCTGCTGTGCGCGCTGACAGGTCCGGGATGCTGTGTCTCC	960
QY	961	CGGTGTGGTGTCTATTCCTGAAATCTCCCGATGGCTGAATCTCCAGGAAGATTTAAG	1020
Db	961	CGGTGTGGTGTCTATTCCTGAAATCTCCCGATGGCTGAATCTCCAGGAAGATTTAAG	1020
QY	1021	AGGCTGAAGATATCATCCAAAAGCTGCAAAAATGACACACAGACTGTACAGACATGA	1080
Db	1021	AGGCTGAAGATATCATCCAAAAGCTGCAAAAATGACACACATGATGTGTACAGACATGA	1080
QY	1081	TATTTGATTTCTGTGGAGAGCTAAATCCCTCGAAGCAGCAGAAAGCTTTCATTTCTGACCC	1140
Db	1081	TATTTGATTTCTGTGGAGAGCTAAATCCCTCGAAGCAGCAGAAAGCTTTCATTTCTGACCC	1140
QY	1141	TGTTTCAGAGACTCGGAATATTGSCCATTAATGACCAATTATGTCTTTTGTGCTAATGATGCTGA	1200
Db	1141	TGTTTCAGAGACTCGGAATATTGSCCATTAATGACCAATTATGTCTTTTGTGCTAATGATGCTGA	1200
QY	1201	CCTCAGTGGGTACTTTGCTCTGTCCTGTGATGTGCTCTTAATTTACATGAGAGATGCTAAC	1260
Db	1201	CCTCAGTGGGTACTTTGCTCTGTCCTGTGATGTGCTCTTAATTTACATGAGAGATGCTAAC	1260
QY	1261	TGAACGTGTTCTCTCTGCTGCTTGTGATGAAATTTCCAGCTTACATTTACAGCTGGCTGAT	1320
Db	1261	TGAACGTGTTCTCTCTGCTGCTTGTGATGAAATTTCCAGCTTACATTTACAGCTGGCTGAT	1320

QY	1321	GGGACAGCGGCCCGGCGTTATATCAATAGCTGCGAGTCTGCTGGGGAGGAGGTGCG	1380
Db	1321	TGGACACCTGGCCAGCGGTTATATCAATAGCTGCGAGTCTGCTGGGGAGGAGGTGCG	1380
QY	1381	TTCTCTTCATTCACACTGGTACTGCTGGATTATTAATCTTATTCATTTGGTCTGGTCAATGC	1440
Db	1381	TTCTCTTCATTCACACTGGTACTGCTGGATTATTAATCTTATTCATTTGGTCTGGTCAATGC	1440
QY	1441	TGGGAAAAATTTGGGATCACTCTGCTTTCTTCATGCTGTATGTCTTTACATGCTGAGCTCT	1500
Db	1441	TGGGAAAAATTTGGGATCACTCTGCTTTCTTCATGCTGTATGTCTTTACATGCTGAGCTCT	1500
QY	1501	ACCCAAACCTGTGAGAACATGCGGGTGGGGGTACATCCAGCGGCTCCAGATGGGGCA	1560
Db	1501	ACCCAAACCTGTGAGAACATGCGGGTGGGGGTACATCCAGCGGCTCCAGATGGGGCA	1560
QY	1561	GCATCATTGCCCCCTACTTGTGTTTAACTCGGTGCTTACACAGATGCTGCGCTTACATCG	1620
Db	1561	GCATCATTGCCCCCTACTTGTGTTTAACTCGGTGCTTACACAGATGCTGCGCTTACATCG	1620
QY	1621	TCATGGGTAGTCTACATGCTCCGTGATTTGGAAATCTTACACCTTTTTCCTCGAAAGTTGG	1680
Db	1621	TCATGGGTAGTCTACATGCTCCGTGATTTGGAAATCTTACACCTTTTTCCTCGAAAGTTGG	1680
QY	1681	GAATGACTCTTCCAGAAAACCTTAGAGCAGATGCGAAAAGTGAATGGTTGAGATCTGGGA	1740
Db	1681	GAATGACTCTTCCAGAAAACCTTAGAGCAGATGCGAAAAGTGAATGGTTGAGATCTGGGA	1740
QY	1741	AAAAAACAGAGACTCAATGAGACACAGAAAAATCCCAAGTCTTAATACTGCATTTCT	1800
Db	1741	AAAAAACAGAGACTCAATGAGACACAGAAAAATCCCAAGTCTTAATACTGCATTTCT	1800
QY	1801	GAATAAATATCTTACCCCATTTGGTGAAGTGAAGAAAAACAGAAAAATAGACCTGTGGAGAA	1860
Db	1801	GAATAAATATCTTACCCCATTTGGTGAAGTGAAGAAAAACAGAAAAATAGACCTGTGGAGAA	1860
QY	1861	ATTCGTTGTTCCCACTGAAATGACGTGACTGTAAACGATGACACCAAAATGAACTTGCT	1920
Db	1861	ATTCGTTGTTCCCACTGAAATGACGTGACTGTAAACGATGACACCAAAATGAACTTGCT	1920
QY	1921	ATCAAGAAATCTGCTCATATACAGTAACCTGCGATGATCTCTGAGATTAATGTCCTTGCT	1980
Db	1921	ATCAAGAAATCTGCTCATATACAGTAACCTGCGATGATCTCTGAGATTAATGTCCTTGCT	1980
QY	1981	TTACAAACCAACCAATTTCTAGAGAGTCTCTTACTATTAATTAATGAATGAGATTGGT	2040
Db	1981	TTACAAACCAACCAATTTCTAGAGAGTCTCTCTTACTATTAATTAATGAATGAGATTGGT	2040
QY	2041	AAGATGCTTAAACAACTGATGTCAGAGGATGGTAAAAATCAATTAAGATTAACTG	2100
Db	2041	AAGATGCTTAAACAACTGATGTCAGAGGATGGTAAAAATCAATTAAGATTAACTG	2100
QY	2101	ATTTCCAATCATACAAATACTATCTCAATAATAAAAT	2135
Db	2101	ATTTCCAATCATACAAATACTATCTCAATAATAAAAT	2135
RESULT 2			
US-10-327-189-1			
: Sequence 1, Application US/10327189			
: GENERAL INFORMATION:			
: APPLICANT: Pelekova, Yanya D			
: APPLICANT: Wintle, Richard F			
: APPLICANT: Rubin, Laurence A			
: APPLICANT: Peter, St George-Hyslop H			
: TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOC			
: FILE REFERENCE: EILP-020			
: CURRENT APPLICATION NUMBER: US/10/327,189			
: CURRENT FILING DATE: 2002-12-20			
: PRIOR APPLICATION NUMBER: 60/362,700			
: PRIOR FILING DATE: 2002-03-08			

;; PRIOR APPLICATION NUMBER: 60/343,338  
;; PRIOR FILING DATE: 2001-12-21  
;; PRIOR APPLICATION NUMBER: 60/427,529  
;; PRIOR FILING DATE: 2002-11-19  
;; PRIOR APPLICATION NUMBER: 60/362,717  
;; PRIOR FILING DATE: 2002-03-08  
;; NUMBER OF SEQ ID NOS: 42  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1  
;; LENGTH: 2214  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (166)..(1821)  
;; OTHER INFORMATION:  
US-10-327-189-1

Query Match 99.8%; Score 2130.2; DB 15; Length 2214;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2132; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCGGCTTCGCGCCCAATTTCTACAGCCTGCTGCCCGGGAACTTCTACATC 60  
DB 20 CCCGGCTTCGCGCCCAATTTCTACAGCCTGCTGCCCGGGAACTTCTACATC 79  
QY 61 CTGGGGAGCGCCAGCTACAGACACTGTCTGAGAAAGCTGTACACCGTAGT 120  
DB 80 CTGGGGAGCGCCAGCTACAGACACTGTCTGAGAAAGCTGTACACCGTAGT 139  
QY 121 CAAGTTTGGAGAGCGGCACTGGGAAACATCGGGAGCTACAGAGAGTGTCCCTCTG 180  
DB 140 CAAGTTTGGAGAGCGGCACTGGGAAACATCGGGAGCTACAGAGAGTGTCCCTCTG 199  
QY 181 GCGAGTGGGGGCTTCAGGCGCTCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
DB 200 GCGAGTGGGGGCTTCAGGCGCTCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 259  
QY 241 ATGGCTTCATAGTATGTACGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 300  
DB 260 ATGGCTTCATAGTATGTACGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 319  
QY 301 TGGCGGAGCGCGCAACTGAGACAGCGCTGGCGCAACAGATGTCCCGCTGGCGCTGC 360  
DB 320 TGGCGGAGCGCGCAACTGAGACAGCGCTGGCGCAACAGATGTCCCGCTGGCGCTGC 379  
QY 361 GGGAGGCGCGGAGGTGCGCCACAGCTCAGCCGCTACCGGCTGGCGCAACTGCGCAACT 420  
DB 380 GGGAGGCGCGGAGGTGCGCCACAGCTCAGCCGCTACCGGCTGGCGCAACTGCGCAACT 439  
QY 421 TCTCGGCGCTGGGGGCTGGAGCGGGGCGCGAGCTGGAGCTGGGGAGCTGGAGGAGA 480  
DB 440 TCTCGGCGCTGGGGGCTGGAGCGGGGCGCGAGCTGGAGCTGGGGAGCTGGAGGAGA 499  
QY 481 GCTGCTGATGGCTGGAGGTTCAAGCAGAGCTGTACCTGTCCACCGTCTGTGACCGAGT 540  
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QY 541 GGAATCTGTGTGTAGAGACAACCTGGAAGGTGCCCTTACCACTCCCTGTTCTTCTAG 600  
DB 560 GGAATCTGTGTGTAGAGACAACCTGGAAGGTGCCCTTACCACTCCCTGTTCTTCTAG 619  
QY 601 GCGTCTCTCGGCTCTTCTGCTCGGGGAGCTGTACAGAGGTTGGGAGGAAGAG 660  
DB 620 GCGTCTCTCTCGGCTCTTCTGCTCGGGGAGCTGTACAGAGGTTGGGAGGAAGAG 679  
QY 661 TTTCTTTCGCAACATGAGCTGTACAGCTGCTTACGCTTCTGTGAGATTTTCTCATCA 720  
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QY 721 GCTGGGAGATGTTCACTGTGTATTTGTATCTGCTGTGGGAGTGGGCAAGTCTCAACTATG 780  
DB 740 GCTGGGAGATGTTCACTGTGTATTTGTATCTGCTGTGGGAGTGGGCAAGTCTCAACTATG 799

QY 781 TGGTAGCCTTCATCTAGGAAGAAATTTGGCAAGTCAGTTCGATTAATCTCTA 840  
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QY 841 CATTAGAGTGTACACATTTTGGAGTTGGCTATATGCTGTCCACCTGTTTGTACT 900  
DB 860 CATTAGAGTGTACACATTTTGGAGTTGGCTATATGCTGTCCACCTGTTTGTACT 919  
QY 901 TCATCAGAGACTGGCGATCTGCTGTGGCGCTGACGGTCCGGAGAGTGTGTCTC 960  
DB 920 TCATCAGAGACTGGCGATCTGCTGTGGCGCTGACGGTCCGGAGAGTGTGTCTC 979  
QY 961 CGCTGTGGTTCATCTCCGAATTCGCCGATGGCTGATATCCAGAGAATTTAGAG 1020  
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QY 1201 CCTCAGTGGTTACTTGTCTGTCTGTGATGCTCTTAATTTACATGAGATGCTTACC 1260  
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QY 1261 TGAACGTTCCTCTCTGCTCTGCTGATGAATTCACAGCTTACAGCTGCTGCTAT 1320  
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QY 1321 TGGCAAGCTGCGCAGCGCTTATATCATACCTCAGTACTGTTCTGGGAGAGAGTGTGC 1380  
DB 1340 TGGCAAGCTGCGCAGCGCTTATATCATACCTCAGTACTGTTCTGGGAGAGAGTGTGC 1399  
QY 1381 TTTCTTCATTCAACTGTGATCTGTGATTTACTTCTTATTCATTGGTGTGATGC 1440  
DB 1400 TTTCTTCATTCAACTGTGATCTGTGATTTACTTCTTATTCATTGGTGTGATGC 1459  
QY 1441 TGGGAAAATTTGGGATACCTGTCTTTCATGCTGTATGTCTTCACTGCTGACTCT 1500  
DB 1460 TGGGAAAATTTGGGATACCTGTCTTTCATGCTGTATGTCTTCACTGCTGACTCT 1519  
QY 1501 ACCCAACCTGTGTACAGGAATGAGCGGTGGGGTCAACATCCAGGCTCCAGAGTGGGA 1560  
DB 1520 ACCCAACCTGTGTACAGGAATGAGCGGTGGGGTCAACATCCAGGCTCCAGAGTGGGA 1579  
QY 1561 GCATCATTTGCCCTTACTTGTTTTACCTGCTGTCTTACAACAGAAATGTCCTACATCG 1620  
DB 1580 GCATCATTTGCCCTTACTTGTTTTACCTGCTGTCTTACAACAGAAATGTCCTACATCG 1639  
QY 1621 TCATGGGTATGTGACGTCTGTGATTTGGAATCTTCACTCTTTTTCCTGAAAGTTTG 1680  
DB 1640 TCATGGGTATGTGACGTCTGTGATTTGGAATCTTCACTCTTTTTCCTGAAAGTTTG 1699  
QY 1681 GAATGACTTCTTCAGAAACCTTGAAGCAGATGAGAAAAGTGAATGGTTACATCTGGGA 1740  
DB 1700 GAATGACTTCTTCAGAAACCTTGAAGCAGATGAGAAAAGTGAATGGTTACATCTGGGA 1759  
QY 1741 AAAAACAAGAGACTCAATGAGAGACAGAGAAAATCCCAAGTTCTAATACTGACTTCT 1800  
DB 1760 AAAAACAAGAGACTCAATGAGAGACAGAGAAAATCCCAAGTTCTAATACTGACTTCT 1819  
QY 1801 GAAAAAATATCTACCCCATTTGGTGAAGTGAAGTAAAAAAGAAAAATAGACCTCTGAGAA 1860  
DB 1820 GAAAAAATATCTACCCCATTTGGTGAAGTGAAGTAAAAAAGAAAAATAGACCTCTGAGAA 1879

QY	1861	TTTGTGTTGCCACCTGAAATGAGCTGCTCTAAGCATTTGACACCAAAATGACCTTGGT	1920
Db	1880	ATTGTGTTGCCACCTGAAATGAGCTGCTCTAAGCATTTGACACCAAAATGACCTTGGT	1939
QY	1921	ATCAAGAAATGCTGCTATACAGTAAACTGATGATTTCTTCAGATAATGTCCTTGGT	1980
Db	1940	ATCAAGAAATGCTGCTATACAGTAAACTGATGATTTCTTCAGATAATGTCCTTGGT	1999
QY	1981	TTACAAACCAACCACTTCTTAGAGCTCTCCTTACTCATTTAATTGAATGATTTGGT	2040
Db	2000	TTACAAACCAACCACTTCTTAGAGCTCTCCTTACTCATTTAATTGAATGATTTGGT	2059
QY	2041	AAGATGCTCTTGAAACAATGTTAGTCAAGAGACTGGTAAATACATATAAAGATTAAACCTC	2100
Db	2060	AAGATGCTCTTGAAACAATGTTAGTCAAGAGACTGGTAAATACATATAAAGATTAAACCTC	2119
QY	2101	ATTTCGAATCATACAATACTATCCCAATAATAAAT	2135
Db	2120	ATTTCGAATCATACAATACTATCCCAATAATAAAT	2154

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1 RESULT 3
2 US-10-327-189-37
3 Sequence 37, Application US/10327189
4 GENERAL INFORMATION:
5 APPLICANT: Pellekova, Vanya D
6 APPLICANT: Wintle, Richard F
7 APPLICANT: Rubin, Laurence A
8 APPLICANT: Peter, St George-Hyslop H
9 APPLICANT: Simionovitch, Katherine A
10 TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIATED WITH INFLAMMATORY BOWEL DISORDERS
11 FILE REFERENCE: ELLP-020
12 CURRENT APPLICATION NUMBER: US/10/327,189
13 CURRENT FILING DATE: 2002-12-20
14 PRIOR APPLICATION NUMBER: 60/362,700
15 PRIOR FILING DATE: 2002-03-08
16 PRIOR APPLICATION NUMBER: 60/343,338
17 PRIOR FILING DATE: 2001-12-21
18 PRIOR APPLICATION NUMBER: 60/427,529
19 PRIOR FILING DATE: 2002-11-19
20 PRIOR APPLICATION NUMBER: 60/362,717
21 PRIOR FILING DATE: 2002-03-08
22 NUMBER OF SEQ ID NOS: 42
23 SOFTWARE: PatentIn version 3.1
24 SEQ ID NO 37
25 LENGTH: 2136
26 TYPE: DNA
27 ORGANISM: Homo sapiens
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31 OTHER INFORMATION: n can be a or t or g or c
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50 LOCATION: (326)..(326)
51 OTHER INFORMATION: n can be a or t or g or c

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47 LOCATION: (2105)..(2105)
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Query Match	98.5%;	Score 2103.4;	DB 15;	Length 2136;
Best Local Similarity	99.0%;	Pred. NO. 0;		
Matches 2115;	Conservative 1;	Mismatches 19;	Indels 1;	Gaps 1
QY	1	CCCCGGCTTCGCGCCCAATTTCTTACAGCCTGCTGCTCCCGGGAGACGTTCTTACATC	60	
Db	1	CCCNMNTTTCGGCGCCCAATTTCTTACAGCCTGCTGCTCCCGGGAGACGTTCTTACATC	60	
QY	61	CTTGGGGAGCGGCCCGAGCTACAGAAGCATGTGTCCTGGAAGAGCTGTATACCCGTAATTG	120	
Db	61	CTTGGGGAGCGGCCCGAGCTACAGAAGCATGTGTCCTGGAAGAGCTGTATACCCGTAATTG	120	
QY	121	CAAGTTTCGAGACGGGACATGTGGAAACATGCGGACCTACGACGAGGTGATCGCCCTTCG	180	
Db	121	CAAGTTTCGAGACGGGACATGTGGAAACATGTGCGGACCTACGACGAGGTGATCGCCCTTCG	180	
QY	181	GGAGATGGGGGGCCCTTCAGGCGCCATCTTCTTCGTCACACGGCAGCATATATCCCA	240	
Db	181	GGAGATGGGGGGCCCTTCAGGCGCCATCTTCTTCGTCACACGGCAGCATATATCCCA	240	
QY	241	ATGCGTTCAATGTATGTCAATCGTGTCTTGGCGGGAGCCCGGAGACACGCTGTGAG	300	
Db	241	ATGCGTTCAATGTATGTCAATCGTGTCTTGGCGGGAGCCCGGAGACACGCTGTGAG	300	



QY 1 CCCCAGCTGCGCCGCAATTTCTAACAGCCTGCTGCTCCCGGAGAGTTCATCATC 60  
Db 1 CCCCAGCTGCGCCGCAATTTCTAACAGCCTGCTGCTCCCGGAGAGTTCATCATC 60  
QY 61 CTTGGGAGGCGCCCAAGCTACAAAGACACTGCTGTGAAAGCGTGTATCAACCGTAGTTG 120  
Db 61 CTTGGGAGGCGCCCAAGCTACAAAGACACTGCTGTGAAAGCGTGTATCAACCGTAGTTG 120  
QY 121 CAAGTTTCGAGGCGGAGTGGGAGACATGGGAGACATGCGAGAGTGTATGCTTCTCTGG 180  
Db 121 CAAGTTTCGAGGCGGAGTGGGAGACATGGGAGACATGCGAGAGTGTATGCTTCTCTGG 180  
QY 181 GCGAGTGGGCGCCCTTCCAGCGGCTCATCTTCTGCTCAGCGGAGAGTATCCCA 240  
Db 181 GCGAGTGGGCGCCCTTCCAGCGGCTCATCTTCTGCTCAGCGGAGAGTATCCCA 240  
QY 241 ATGGCTTCATATGATATGATGCTGTCTGTGCGGGGAGCCCGGAGACCGCTGTGAG 300  
Db 241 ATGGCTTCATATGATATGATGCTGTCTGTGCGGGGAGCCCGGAGACCGCTGTGAG 300  
QY 301 TGGCGGAGCGCGGCAACCTGAGAGCGGCTGGGCAACAAGTGTCCGGTGGGCTGCG 360  
Db 301 TGGCGGAGCGCGGCAACCTGAGAGCGGCTGGGCAACAAGTGTCCGGTGGGCTGCG 360  
QY 361 GGGAGCGCGCGAGGTGCGCCACAGCTGACCGGCTACCGGCTGCGGACCATGCGCACT 420  
Db 361 GGGAGCGCGCGAGGTGCGCCACAGCTGACCGGCTACCGGCTGCGGACCATGCGCACT 420  
QY 421 TCTCGGCGCTCGGGGCTGGAGCGGGGCGGAGAGTGTGAGAGTGTGAGAGAGAGA 480  
Db 421 TCTCGGCGCTCGGGGCTGGAGCGGGGCGGAGAGTGTGAGAGTGTGAGAGAGAGA 480  
QY 481 GCTGCTGATGAGTGGGAGTTCAGCCAGAGCTGACCTGTCACCGCTGAGCGAGT 540  
Db 481 GCTGCTGATGAGTGGGAGTTCAGCCAGAGCTGACCTGTCACCGCTGAGCGAGT 540  
QY 541 GGAATCGGTGTGAGGACAACCTGGAAGTGTGCTTCAACACTTCTTCTGTG 600  
Db 541 GGAATCGGTGTGAGGACAACCTGGAAGTGTGCTTCAACACTTCTTCTGTG 600  
QY 601 GCGTGTCTCGGCTCTCTCTGCTGTCGGGAGCTGTACAGAGTGTGAGAGAGAG 660  
Db 601 GCGTGTCTCGGCTCTCTCTGCTGTCGGGAGCTGTACAGAGTGTGAGAGAGAG 660  
QY 661 TTTCTCTTCCCAACCATGCTGTACAGAGTGTGCTTCTGAGATTTCTTCATCA 720  
Db 661 TTTCTCTTCCCAACCATGCTGTACAGAGTGTGCTTCTGAGATTTCTTCATCA 720  
QY 721 GCTGGAGAGTTCATGTTATTTGTCATGCTGGGCAATGGGCAAGATCTCAACTATG 780  
Db 721 GCTGGAGAGTTCATGTTATTTGTCATGCTGGGCAATGGGCAAGATCTCAACTATG 780  
QY 781 TGGTACCTTCACTACTAGAGACAGAAATCTTGGCAAGTGTGTATATATCTCTA 840  
Db 781 TGGTACCTTCACTACTAGAGACAGAAATCTTGGCAAGTGTGTATATATCTCTA 840  
QY 841 CATTAGAGATGTGCACATTTTTCAGAGTGTGCTATATGCTGTGCTGCTACT 900  
Db 841 CATTAGAGATGTGCACATTTTTCAGAGTGTGCTATATGCTGTGCTGCTACT 900  
QY 901 TCATCGAGACTGGGAGATGCTGCTGCGGCTACAGCTGTGCGGAGTGTGCTGCT 960  
Db 901 TCATCGAGACTGGGAGATGCTGCTGCGGCTACAGCTGTGCGGAGTGTGCTGCT 960  
QY 961 CGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969  
Db 961 CGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969  
QY 970 GCTATGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
Db 970 GCTATGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
QY 1021 GACTTGGCCCAAGAGGCGAGCCTGGGAGCAGCACTGACAGTGTGCTGCTGCTGCTGCT 1080

QY 970 ----- 969  
Db 1081 AACATTACAGTGTCTTACCATTTTCTTATAAAGAAATAGCTTCTTCTGAGATC 1140  
QY 970 ----- 969  
Db 1141 CCATCTGGGAGGTTCATCTCTGATATCTCCCGGATGGCTGTATCCAGAGAGATTTA 1200  
QY 1018 GAGAGGCTGAGATATTCATCCAAAAGCTGCAAAAATGTAACACAGCTGTACAGCAG 1077  
Db 1201 GAGAGGCTGAGATATTCATCCAAAAGCTGCAAAAATGTAACACAGCTGTACAGCAG 1260  
QY 1078 TGAATTTGATTTCTGTGAGAGAGCTAAATCCCTGAACAGAGAGAAAGCTTCAATTCG 1137  
Db 1261 TGAATTTGATTTCTGTGAGAGAGCTAAATCCCTGAACAGAGAGAAAGCTTCAATTCG 1320  
QY 1138 ACCTGTACAGACTGCGAATATTTGCCATATGACCATTTATGCTTGTGCTGATGATGC 1197  
Db 1321 ACCTGTACAGACTGCGAATATTTGCCATATGACCATTTATGCTTGTGCTGATGATGC 1380  
QY 1198 TGACCTGAGTGGTACTTGTCTGTCTGTGATGCTGCTATATTTACATGAGATGCT 1257  
Db 1381 TGACCTGAGTGGTACTTGTCTGTCTGTGATGCTGCTATATTTACATGAGATGCT 1440  
QY 1258 ACCTGAATGTTTCTCTCTGCTGATTTGAATTTCCAGCTTACATTTACAGCTGTGCTG 1317  
Db 1441 ACCTGAATGTTTCTCTCTGCTGATTTGAATTTCCAGCTTACATTTACAGCTGTGCTG 1500  
QY 1318 TATTGCGAAGCTGCGCCAGCGGTTATATCATAGCTGCAGTACTTCTGGGAGAGAGTG 1377  
Db 1501 TATTGCGAAGCTGCGCCAGCGGTTATATCATAGCTGCAGTACTTCTGGGAGAGAGTG 1560  
QY 1378 TGCTTCTCTTCAATCACTGATGATGATTTATTTATTTATTTATTTATTTATTTATTT 1437  
Db 1561 TGCTTCTCTTCAATCACTGATGATGATTTATTTATTTATTTATTTATTTATTTATTT 1620  
QY 1438 TGCTGGGAAATTTGGGATCATCTGTCTTCTCATAGCTGTATGCTTCACTGCTGAGC 1497  
Db 1621 TGCTGGGAAATTTGGGATCATCTGTCTTCTCATAGCTGTATGCTTCACTGCTGAGC 1680  
QY 1498 TCTACCCAAACCTGTGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1557  
Db 1681 TCTACCCAAACCTGTGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740  
QY 1558 GCAGCATATTTGCCCCACTTGTGTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1617  
Db 1741 GCAGCATATTTGCCCCACTTGTGTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
QY 1618 TCGTCATGGGATGCTGACTGCTGTGATTTGGAATCTTACCCCTTTTCTGGAAGTT 1677  
Db 1801 TCGTCATGGGATGCTGACTGCTGTGATTTGGAATCTTACCCCTTTTCTGGAAGTT 1860  
QY 1678 TGGGAATGACTCTTCCAGAAACCTTAGAGAGATGCGAAGTGAATGGTTCAGATCTG 1737  
Db 1861 TGGGAATGACTCTTCCAGAAACCTTAGAGAGATGCGAAGTGAATGGTTCAGATCTG 1920  
QY 1738 GGAAGAAACAGAGACTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1797  
Db 1921 GGAAGAAACAGAGACTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
QY 1798 TCTGAAAAATATTTACCCATTTTGTGAAAGTGAAGAGAGAGAGAGAGAGAGAGAG 1857  
Db 1981 TCTGAAAAATATTTACCCATTTTGTGAAAGTGAAGAGAGAGAGAGAGAGAGAGAG 2040  
QY 1858 GAAATTTGTTTCCCTGCAAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAAT 1917  
Db 2041 GAAATTTGTTTCCCTGCAAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAAT 2100  
QY 1918 GCTATCAAGAAATGCTGCTATACAGTAACTGTGATGATTTCTTCCAGATATGCTCT 1977  
Db 2101 GCTATCAAGAAATGCTGCTATACAGTAACTGTGATGATTTCTTCCAGATATGCTCT 2160  
QY 1978 GCTTTACAAACCAACATTTTCTAGAGAGTCTCTTACTCATTTATTTCAATGAAATG 2037





Db 1681 TCTACCAACCTTGTGAGGACATGCGGTGGGGGACATCCAGGCGCTCCAGAGTGG 1740  
QY 1558 GCAGCATCATTTGCCCTTACTTTGTCTTACCTCGGTGCTTACACAGATGCTCCCTACA 1617  
Db 1741 GCAGCATCATTTGCCCTTACTTTGTCTTACCTCGGTGCTTACACAGATGCTCCCTACA 1800  
QY 1618 TCGCATGGGTAGTGTACTGTCTGTATTTGGAATCTTCAACCTTTTTCCTGAAAGTT 1677  
Db 1801 TCGCATGGGTAGTGTACTGTCTGTATTTGGAATCTTCAACCTTTTTCCTGAAAGTT 1860  
QY 1678 TGGGAATGACTCTTCCGAAACCTTAGAGAGATGCGAAGTGAATGGTTAGATCG 1737  
Db 1861 TGGGAATGACTCTTCCGAAACCTTAGAGAGATGCGAAGTGAATGGTTAGATCG 1920  
QY 1738 GGAAGAAACAGAGACTCAATGAGACAGAGAGAAATCCAGAGTCTTAATACATCAT 1797  
Db 1921 GGAAGAAACAGAGACTCAATGAGACAGAGAGAAATCCAGAGTCTTAATACATCAT 1980  
QY 1798 TCTGAAAAAATATCTACCCCATTTGGTGAAGTGAAGAAACGAAAAATAGACCTGTGA 1857  
Db 1981 TCTGAAAAAATATCTACCCCATTTGGTGAAGTGAAGAAACGAAAAATAGACCTGTGA 2040  
QY 1858 GAAATTCGTGTTCCGACCTGAATGAGACGTCGTAGACGATGACACCAAAATGAACTT 1917  
Db 2041 GAAATTCGTGTTCCGACCTGAATGAGACGTCGTAGACGATGACACCAAAATGAACTT 2100  
QY 1918 GCTATCAAGAAATGCTGTCATACAGTAAACTCTGATGATTTCTTCAGATATGCTCT 1977  
Db 2101 GCTATCAAGAAATGCTGTCATACAGTAAACTCTGATGATTTCTTCAGATATGCTCT 2160  
QY 1978 GCTTTCACCAACCAACCATTTCTAGAGAGTCTCTTACTATTAATCAATGAATGAT 2037  
Db 2161 GCTTTCACCAACCAACCATTTCTAGAGAGTCTCTTACTATTAATCAATGAATGAT 2220  
QY 2038 GGTAGATGTCTGAAACATGTTAGTCAAGAGTCTGTAAGTAAATACATATAAGATTACA 2097  
Db 2221 GGTAGATGTCTGAAACATGTTAGTCAAGAGTCTGTAAGTAAATACATATAAGATTACA 2280  
QY 2098 CTCATTTCCATATCATCAATTAATCAATTAATTAAT 2135  
Db 2281 CTCATTTCCATATCATCAATTAATCAATTAATTAAT 2318

RESULT 6  
US-10-144-771-9909  
; Sequence 9909, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 9909  
; LENGTH: 2080  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-144-771-9909

Query Match 61.4%; Score 1310.6; DB 14; Length 2080;  
Best Local Similarity 85.7%; Pred. No. 4,4e-303;  
Matches 1470; Conservative 0; Mismatches 239; Indels 6; Gaps 1;

QY 137 AGTGGAGACATGCGGAGCTAGACAGAGTGAATGCGCTCTGCGGAGTGGGCGCTT 196  
Db 109 AGTGGAGACATGCGGAGCTAGACAGAGTGAATGCGCTCTGCGGAGTGGGCGCTT 168  
QY 197 CCAGGCGCTCATCTTCTCTCTGCTAGCGGCCGACATATCCCAATGGCTTCAATGTAT 256  
Db 169 CCAGGCGCTCATCTTCTCTCTGCTAGCGGCCGACATATCCCAATGGCTTCAATGTAT 228  
QY 257 GTCAAGTGTCTCTGCGGCGGAGACCCGAGACGCGTGTGAGAGTCCGGAGCGCGGAA 316

Db 229 GTCAAGTGTCTCTGCGGCGGAGACCCCGAGACACCGTTGCGCTTCTGACATGTGAA 288  
QY 317 CCGAGACACGCGCTGGCGCAACAGATGTCCCGTGGGGCTGCCGAGACGCCGAGAGT 376  
Db 289 CCGAGACACGCGCTGGCGCAACAGATGTCCCGTGGGGCTGCCGAGAGAGAGAGAGT 348  
QY 377 GCCCCAGACCTGACCGCGTACCGGCTGCGCACATGCGCAACTTCTGCGGCGTGGCT 436  
Db 349 GCCCTAGAGCTCCCGCGGTACCGATGCGACATGCGCAACTTCTGCGGATGGGCT 408  
QY 437 GGAGCGGCGCGCGAGCTGTGAGCTGGGCGAGCTGGAGACAGAGAGTCTGATGGCTG 496  
Db 409 GGAGCGGCGCGAGCTGTGAGCTGGGCGAGCTGGAGAGAGAGTCTGATGGCTG 468  
QY 497 GGAGTTCAGCCGACGCTTACCTGTCCACCGCTGTGACCGCGAGTGGATTCGATGTGA 556  
Db 469 GGAGTTCAGCAAGACATCTTCTGTCCACCATCTGTGACAGAGTGGATTCGATGTGA 528  
QY 557 GGACACATGGAAGTGGCCCTGACACCCCTCCCTGTTCTGTGAGGCGTCTCGGCTC 616  
Db 529 GGATGACGTGAAGACACCCCTGACACCCCTCCCTGTTCTGTGAGGCGTCTCGGCTC 588  
QY 617 CTTCGTGTCGCGGCGAGCTGTGACAGAGTGTGGCAGAGAAAGTCTTCTTCCGACCAT 676  
Db 589 CTTCGTGTCGCGGCGAGCTGTGACAGAGTGTGGCAGAGAAAGTCTTCTTCCGACCAT 648  
QY 677 GCGCTTACAGACATGCTTCAAGCTTCCAGATTTTCCCATCAGCTGGGAGATGTTAC 736  
Db 649 GCGCTTACAGACATGCTTCAAGCTTGTGTGACAGATTTTCCATCAGCTGGGAGATGTTAC 708  
QY 737 TGTGTTATTTGTATCGTGGGCGATGGGCGACATGCTCAACTATGTGTGATGCTTCAAT 796  
Db 709 TGTGTTATTTGTATCGTGGGCGATGGGCGACATGCTCAACTATGATGGGCTTCAAT 768  
QY 797 AGGAACAAATTTCTGGCAAGTCAATGCTGATATATCTCTACATTTAGAGTGTGAC 856  
Db 769 AGGAACAAATTTCTGGCAAGTGTGATGCTGATATATCTCTACATTTAGAGTGTGAC 828  
QY 857 ATTTTTCAGTGTGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 916  
Db 829 ATTTTTCAGTGTGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888  
QY 917 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 976  
Db 889 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948  
QY 977 TCTGGAATCTCCCGATGCTGATATCCGAGAGAAATTTAGAGGCTGAAGATATCAT 1036  
Db 949 TCTGGAATCTCCCGATGCTGATATCCGAGAGAAATTTAGAGGCTGAAGATATCAT 1008  
QY 1037 CCAAAAAGCTGCAAAAATGAGACACAGCTGTACCGAGAGTATTTGTTGCTGCTGCTGCT 1095  
Db 1009 CCAAAAAGCTGCAAAAATGAGACACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068  
QY 1096 -----AGAGCTAAATCCCTGGAAGACAGACAGAAAGCTTCAATTTGAGCTGTTCAGGAC 1150  
Db 1069 GCTACAGAGAGCTAAATCTCTGGAAGACAGACAGAAAGCTATTAATCTGAGCTGTTCAGGAC 1128  
QY 1151 TCGGAATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1210  
Db 1129 TCGGAATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188  
QY 1211 TTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270  
Db 1189 TTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248  
QY 1271 CCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1330  
Db 1249 CCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1308  
QY 1331 GCCAGGCGTTATATCATAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1390



Db 1309 GCCACGAGATATATATAGCTGGGGTCTATTCTGGGGAGAGGTGCTTCTTGAT 1368  
 QY 1391 TCACTGGTACCTGGATTTACTTCTTATCCATTTGCTGTGATGCTGGGAAATT 1450  
 Db 1369 CCAATGGTACTGAGATTTAACTTGTGCTCAATGGAGCTGATGCTGGGAAATT 1428  
 QY 1451 TGGGATCACTCTGCTTCTCCATGCTGATGCTTCACTGCTGAGCTTACCCAACT 1510  
 Db 1429 TGGGATCACTCTGCTTCTCCATGCTGATGCTTCACTGCTGAGCTTACCCAACT 1488  
 QY 1511 GGTTCAGGAACATGGCGGTGGGGGTACATCCAGGCTTCCAGATGGGACGATTC 1570  
 Db 1489 GGTTCAGGAACATGGCGGTGGGGGTACATCCAGGCTTCCAGATGGGACGATTC 1548  
 QY 1571 CCCCTACTTGTCTTCTGCTGGGTGCTTACACAGATGCTGCCATCATGCTATGGGTAG 1630  
 Db 1549 CCCCTACTTGTCTTCTGCTGGGTGCTTACACAGATGCTGCCATCATGCTATGGGTAG 1608  
 QY 1631 TCTGACTGCTGATTTGGAATCTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1690  
 Db 1609 TCTGACTGCTGATTTGGAATCTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1668  
 QY 1691 TCCAGAACTTAGAGCAGATGAGCAAAAGTAAAGTTCAGATCTGGGAAAAAACAG 1750  
 Db 1669 ACCAGAGAACTTGGAGCAGATGAGCAAAAGTAAAGTTCAGATCTGGGAAAAAACAG 1728  
 QY 1751 AGACTCAATGAGAGCAGAGAAATCCCAAGTCTTATTAATGCTGATCTGAAAAAATAT 1810  
 Db 1729 AGTCTAGTGGAGCAGAGAAAGCCCAAGTCTTATTAATGCTGATCTGAAAAAATAT 1788  
 QY 1811 CTACCCCATTTGGTGAAGTGAATAACAGAAAAATA 1845  
 Db 1789 CCAAGGCACTTGGCAAACTGAAAGCAGATGATTA 1823  
 RESULT 7  
 US-09-949-016-438  
 ; Sequence 438, Application US/09949016  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: C1001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 438  
 ; LENGTH: 3252  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-438  
 Query Match 49.9%; Score 1065.8; DB 11; Length 3252;  
 Best Local Similarity 77.5%; Pred. No. 2.1e-244;  
 Matches 1305; Conservative 0; Mismatches 372; Indels 6; Gaps 1;

Db 295 TCAGCGCAGCATATCCCAATGGCTTCAACGGGCTGTCTCCGTCTGATATAGCA 354  
 QY 280 CCCCAGACACCGCTGTGAGATGCGGAGCCCGGAACTGAGACGCGCTGGCGAACA 339  
 Db 355 CCCCAGACACCGCTGTGAGATGCGGAGCCCGGAACTGAGACGCGCTGGCGAACC 414  
 QY 340 ACAATGCCGCTGCGGCTGCGGAGCGCGGAGGCGCCGACAGCTGAGCGGCTTACC 399  
 Db 415 ACAATGCCGCTGCGGCTGCGGAGCGCGGAGGCGCCGACAGCTGAGCGGCTTACC 474  
 QY 400 GCGTCGCCACCATGCGCAACTTCTCGGCGCTCGGCGTGGAGCCGCGGCGGAGCGTACC 459  
 Db 475 GCGTCGCCACCATGCGCAACTTCTCGGCGCTCGGCGTGGAGCCGCGGCGGAGCGTACC 534  
 QY 460 TGGGGCAGCTGGAGCAGAGAACTGCTGATGCTGGAGTTCAGGCTGAGAGAGCTTACC 519  
 Db 535 TGGGGCAGCTGGAGCAGAGAACTGCTGATGCTGGAGTTCAGGCTGAGAGAGCTTACC 594  
 QY 520 TGTCCACCGTCGAGCAGAGTGGATCTGCTGCTGGAGCAGCACTGGAAGAGTGCCTCA 579  
 Db 595 TGTCCACCGTCGAGCAGAGTGGATCTGCTGCTGGAGCAGCACTGGAAGAGTGCCTCA 654  
 QY 580 CCACCTCCCTGCTTCTGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 639  
 Db 655 CAATCTCTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 714  
 QY 640 ACAGGTTGGCAGAGAAAGCTTCTCTGCAACCATGCTGTACAGACTGGCTTACGCT 699  
 Db 715 ACAGGTTGGCAGAGAAAGCTTCTCTGCAACCATGCTGTACAGACTGGCTTACGCT 774  
 QY 700 TCTGCAATTTTCTCCATCAGCTGGAGATGCTTCACTGCTTATTTGCTATGCTGAGGA 759  
 Db 775 TCTGCAATTTTCTCCATCAGCTGGAGATGCTTCACTGCTTATTTGCTATGCTGAGGA 834  
 QY 760 TGGGCCAGATCTCCACTATGCTGAGCTTCACTAGCAGAGAAATCTTGGCAAGT 819  
 Db 835 TGGGCCAGATCTCCACTATGCTGAGCTTCACTAGCAGAGAAATCTTGGCAAGT 894  
 QY 820 CAGTGGTATTAATTTCTACATTTAGAGTGGAGTGGACATTTTGGAGTGGCTATATGC 879  
 Db 895 CAGTGGTATTAATTTCTACATTTAGAGTGGAGTGGACATTTTGGAGTGGCTATATGC 954  
 QY 880 TGTGCGCAGTGTGCTTACTTCAATGAGAGCTGGGAGTGTGCTGCTGCGCTGACG 939  
 Db 955 TGTGCGCAGTGTGCTTACTTCAATGAGAGCTGGGAGTGTGCTGCTGCGCTGACG 1014  
 QY 940 TGGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 999  
 Db 1015 TGGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074  
 QY 1000 TATCCAGAGAAATTTAGAGAGCTGAAATATCATCCAAAAGCTGCAAAAATGACA 1059  
 Db 1075 TATCCAGAGAAATTTAGAGAGCTGAAATATCATCCAAAAGCTGCAAAAATGACA 1134  
 QY 1060 ACACAGCTGACAGCAGTATTTGATTTCTGTGAG-----GAGCTAAATCCCTCA 1113  
 Db 1135 GATTTGTTGCTTCCACTATCTTGGACCGAGTGAATTAACAAGCTAAGTTCCAAAG 1194  
 QY 1114 AGCAGCAGAAAGCTTCAATCTGAGCTGTTCAGAGCTGGGAATATTCATATATACA 1173  
 Db 1195 AGCAGCAGAAAGCTTCAATCTGAGCTGTTCAGAGCTGGGAATATTCATATATACA 1254  
 QY 1174 TTAATGCTTGTGCTATGATGATGCTGACCTCACTGAGGTTACTTGTGCTGCTGATG 1233  
 Db 1255 TTAATGCTTGTGCTATGATGATGCTGACCTCACTGAGGTTACTTGTGCTGCTGATG 1314  
 QY 1234 CTCCTAATTTACATGAGATGCTTACCTGAAGTCTTCTGCTGCTGATTAATTC 1293  
 Db 1315 CTCCTAATTTACATGAGATGCTTACCTGAAGTCTTCTGCTGCTGATTAATTC 1374  
 QY 1294 CAGCTTAACATTAAGCTGCTGCTTATTTGAGAGCTGCGCAGGCTTATATATAGCTG 1353  
 Db 1375 CAGCTTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1434



Db	1255	TCATGTCATTAATGCTGTGGATGACCAATATACAGTGGGCTATTTTGGGCTTTCGGCTTGATA	1314
QY	1234	CTCCTAAATTACATGAGAGATCCCTAACCTGAACCTGTTTCCTCTCCCTCGCTTGAATGAAATTC	1293
Db	1315	CTCTCACTTCGATGGGGACATCTTTGGAACTGCTTCCTTTTCAGCGAATGGTTGAAGTCC	1374
QY	1294	CAGCTTACATTAACAGCCCTGGCTGGCTATTGGCAAGCGCTGCCAGGCGTTATATCATAGCTG	1355
Db	1375	CAGCATATGCTGTGGCCCTGGCTGGCTGCTGCACAAATTTGGCCCCGGCGCATTTCCATGGCCA	1434
QY	1354	CAGTACTGTTCTGGGGAGAGAGTGTGCTTCTTTCATTTCACTGAGTACTGTGATTTATTT	1413
Db	1435	CTGGCCGCTTCCCTGGGTGGGAGTGTCTCTCTCTTCATGCACTGGTACCCCAAGACTTGT	1494
QY	1414	ACTTCTTATATCCATTGGTGTGTGTCATGCTGGGAAAAATTTGGGATCACCCTGCTTTCTCCA	1473
Db	1495	ATTATTTTGGCTACAGTCTCTGGTGTGATGGTGGGCAAGTTTGGAGTACAGGCTCCCTTTCCA	1554
QY	1474	TGCGTATGTCCTACAGTGTAGGTCTTAACCAACCCGTGTAGAGAACATGGCGGTGGGGG	1533
Db	1555	TGCTCTACGTGTACACAGCCGAGCTGTATCCCAAGTGGTGAAGAAACATGGGTGTGGGAG	1614
QY	1534	TCACATCCACAGGCTCCAGAGTGGGAGACATATTGGCCCCCTACTTTTGTTCACCGGTG	1593
Db	1615	TCACCTCCACAGCATCCCGGCTGGGAGACATCCGTCTCCCTACTGTTTACCTTGGTGTG	1674
QY	1594	CTTACAAACAGATCTGCTCCCTACATCGTCATGGGTAGTGTGACGTGCTCGATTTGAAATCT	1653
Db	1675	CCATACGACCGCTTCTCCCTACATCTTCATATGGGAATCTGACCATCTGCACAGCCATCC	1734
QY	1654	TCACCCCTTTTTCCTGGAAGTTTGGGAATGATCTTCCAGAAACCTTAGAGACAGATGC	1713
Db	1735	TCACCTTGTTTCTCCACAGAGACTTGGGTATCCCACTGCCAGAACCATTTGATACCAAGATGC	1794
QY	1714	AGAAAGTGAATGGTTTCAGATCTGGGAAAAAAAACAGAGACTCATATGAGAGACAGAGAAA	1773
Db	1795	TAAAGATCAAAAGAAATGAACAACAGAAAACCTCAATGCACACAAAGATGTTAATAAGTGTG	1854
QY	1774	ATC 1776	
Db	1855	GTC 1857	

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RESULT 9
US-09-949-016-2058
: Sequence 2058, Application US/09949016
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2058
: LENGTH: 3223
: TYPE: DNA
: ORGANISM: Human
: US-09-949-016-2058

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Query Match      47.9%; Score 1023; DB 11; Length 3223;
Best Local Similarity 76.6%; Pred. No. 3.8e-224;
Matches 1289; Conservative 0; Mismatches 370; Indels 24; Gaps 2;

    100 GCCTGTCATCAACCCCTACTTGCAGTTTCGGAGCGGACGTGGGAAACCATCGGGACATCG 159
       ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db	175	CGCGTCCCCGAGCCCCAGGCGCGGCTCTGAGGGCCCTGAGGGCGGCATGCGGACTACG	234
QY	160	ACGAGGTGATCCGCTTCTCTGGGCGAATGGGGGCGCTTCCAGGCGCTCATCTTCTCTGC	219
Db	235	ACGAGGTGACCGCTTCTCTGGGCGAATGGGGGCGCTTCCAGGCGGCATCTTCTCTGC	294
QY	220	TCAGGCGCCAGTCATCCCCAATGGGCTTAATGGTATGTCAGTCGTTCTCTGGGGGA	279
Db	295	TCAGGCGCCAGTCATCCCCAATGGGCTTACCGGCGCTGTCTCTCGGTCTCTGATAGCCA	354
QY	280	CCCCGAGACCGCGTGTGAGTTCGCGGACGCGCGCACTGAGCAGCGCTTGGCGACAA	339
Db	355	CCCCGAGACCGCGTGTGAGTTCGCGGACGCGCGCACTGAGCAGCGCTTGGCGACAA	414
QY	340	ACAGTGTCCCGGTGGGGGTGGGGAGCGCGGAGGTGGCCCACTGTGACGCGGTACG	399
Db	415	ACACTGTCCCACTGGGGGTGGGGAGCGCGCGAGGTGGCCCACTGTGACGCGGTACG	474
QY	400	GGCTCGCCACCATTCGCCAATTCTCGGCGCTCGGGCTGGAGGCCGGGCGCGAGTGGAC	459
Db	475	GGCTCGCCACCATTCGCCAATTCTCGGCGCTCGGGCTGGAGGCCGGGCGCGAGTGGAC	534
QY	460	TGGGGCAGCTGGAGAGAGAGAGACTGCTGCTGGATGCGTGGGAGTTTACCCAGAGCTTACC	519
Db	535	TGGGGCAGCTGGAGAGAGAGAGACTGCTGCTGGATGCGTGGGAGTTTACCTACGAGAGCTTACC	594
QY	520	TGTCCACGCTGCTGACCCGAGTGGAACTTGTTGTGTAGACACATGGAGTGGCCCTCA	579
Db	595	TGTCCACGCTGCTGACCCGAGTGGAACTTGTTGTGTGTAGACACATGGAGTGGCCCTCA	636
QY	580	CCACCTCCCTGTCTTCTGTAAGCGTGTCTCTGGCTCTCTGCTGTCCGGGCGAGTGTGAG	639
Db	637	CATCTCTCTGTCTTCTGTAAGCGTGTCTCTGGCTCTCTGCTGTCTGGGCGAGTGTGAG	696
QY	640	ACAGTGTGGCAGAGAAAGCTTCTCTTCTGCAACACATGGCTGTGACAGTGTGAGTACGT	699
Db	697	ACAGTGTGGCAGAGAAAGCTTCTCTTCTGCAACACATGGCTGTGACAGTGTGAGTACGT	756
QY	700	TCTCGACATTTTCTTCATCAGCTGGGAGAGTTCATCTGTTATTTGTTCATCTGTGGGA	759
Db	757	TCTCGACATTTTCTTCATCAGCTGGGAGAGTTCATCTGTTATTTGTTCATCTGTGGGA	816
QY	760	TGGGCGAGTCTCCAAACTATGTGTAAGCTTATCTACTGTAAGCAAAATTTCTGGCAAT	819
Db	817	TGGGCGAGTCTCCAAACTATGTGTAAGCTTATCTACTGTAAGCAAAATTTCTGGCAAT	876
QY	820	CAGTTTCAATTAATTTCTCTACATTATAGAGTGTGCAACATTTTTCAGATTTGGCTAATGC	879
Db	877	CAGTTTCAATTAATTTCTCTACATTATAGAGTGTGCAACATTTTATATGATTTGGCTAATGC	936
QY	880	TGCTGCCACTGTTTGTCTTAATCATCAGAGACTGGCGGATGCTGCTGTGCGCTGACGG	939
Db	937	TGCTGCCACTGTTTGTCTTAATCATCAGAGACTGGCGGATGCTGCTGTGCGCTGACGCA	996
QY	940	TGCGGGAGTGTGTGTGTCGCCGTGTGGTGTTCATTCCTGAATCTCCCGATGGCTGA	999
Db	997	TGCGGGAGTGTGTGTGTCGCCGTGTGGTGTTCATTCCTGAATCTCCCGATGGCTGA	1055
QY	1000	TATCCAGAGAGATTTAGAGAGGCTGAAGATATATCATCCAAAAGCTGTGCAAAATGACAA	1055
Db	1057	TCTCTCAAGGAGAGATTTAGAGAGGCTGAAGATATATCATCCGAAAGCTGTGCAAAAGCTGA	1111
QY	1060	ACACAGCTGTACACACAGTGAATTTGATTCGTGTGAG-----GAGCTAATTCCTCTGA	1111
Db	1117	GGATTTGTGTGTCTTCCACTATCTTTGACCCGAGTGAAGTTCACAAACCTCAATCTTCACGA	1177
QY	1114	AGCAGCAGAAAGCTTTCATCTTGGACCTGTTCAGAGCTGCGAATATTTGCCAATATGACCA	1177
Db	1177	AGCAGCAGTCCOACAAACATCTGTGATCTGTCTTCGAACTGGAAATTTCCGGATGTGCACCA	1233
QY	1174	TTATGTCTTGTCTGTATGATGCTGACCTCAGTGTGGTTTACTTGTCTGTCTGTGATG	1233
Db	1237	TCATGTTCATATGCTGTGTGATGACCAATATAGTGTGGCTAATTTTGGCTTTCGCTTGATA	1299

[illegible]





1477 ATATTGGCTACAGTCTGGTGTATGGTGGCAAGTTTGGAGTTCACGCGTCTTTTCCA 1536  
1474 TGCTGTATGCTTACGCTGAGCTCTACACCAACCCCTGCTCAGAGATATGGCGTGGG 1533  
1337 TGTCTAGCTGTACACGCGCTGATCTCCACAGGTGAGAAATATGGGTGGAG 1596  
1534 TCACATCCACGCGCTCCAGAGTGGGAGCATCATATGCCCCCTACTTGTGTACCTGGT 1593  
1597 TCACCTSCACAGCATCCCGCTGGGAGCATCCCTGCTCTCTACTTGTGTACCTGGT 1556  
1594 CTTCACACAGATCTCTCTCTACATCTGCTATGGTGTGCTGCTGCTGATTTGAAT 1653  
1657 CTTACGACCGCT 1716  
1654 TCACCT 1713  
1717 TCACCT 1776  
1714 AGAAAGTGAATGTTTCTGATCTGGGAAAAAACAAGACTCATATGAGACAGAA 1773  
1777 TAAAGTCAAAAGATGAACACAGAAATCTCAAGTACACACAGATGTAAAGATG 1836  
1774 ATC 1776  
1837 GTC 1839

RESULT 12  
Sequence 4827, Application US/60453050  
GENERAL INFORMATION:  
APPLICANT: CARLIL, Michele  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CU01457  
CURRENT FILING DATE: 2003-03-10  
NUMBER OF SEQ ID NOS: 82762  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4827  
LENGTH: 3223  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-453-050-4827

Query Match 47.6% Score 1016.2; DB 18; Length 3223;  
Best Local Similarity 75.6%; Pred. No. 1.6e-232;  
Matches 1272; Conservative 17; Mismatches 370; Indels 24; Gaps 2;

100 CGCTGTCATACCCGTAAGTTTGGAGCGGCACTGGAGATGCGGACTAG 159  
175 CGGGTTCGCGACCCGCGCGCTCTGTGGGCTCTGAGGGCGGATGCGGACTAG 234  
160 ACGAGTATCGGCTCTGGGAGGAGGGGCGCTTCCAGGCGCTCATCTTCTCTG 219  
235 ACGAGTATCGGCTCTGGGAGGAGGGGCGCTTCCAGGCGCTCATCTTCTCTG 294  
220 TCAAGCGACATATCCCAATGAGTTCATATGATGATGATGATGATGATGATGATG 279  
295 TCAAGCGACATATCCCAATGAGTTCATATGATGATGATGATGATGATGATGATG 354  
280 CCGCGAGACCGCTCTGAGTCCGAGCGCGGAGACTGAGACAGCGGCTGGCGACA 339  
355 CCGCGAGACCGCTCTGAGTCCGAGCGCGGAGACTGAGACAGCGGCTGGCGACA 414  
340 ACGAGTATCGGCTCTGGGAGGAGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 399  
415 ACGAGTATCGGCTCTGGGAGGAGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474  
400 GCGTCCACATCGCAATCTCTGCGGCTGCGGCTGAGGCGGGGCGAGCTGAGAC 459

475 GCGTCCACATCGCAATCTCTGCGGCTGCGGCTGAGGCGGGGCGGAGCTGAGAC 534  
460 TGGGAGAGCTGAGAGAGAGAGAGCTGCTGATGCTGGAGGATTCAGCCAGAGCTTACC 519  
535 TGGGAGAGCTGAGAGAGAGAGAGCTGCTGATGCTGGAGGATTCAGCCAGAGCTTACC 594  
520 TGTCCACGCTGAGAGAGAGAGAGCTGCTGATGCTGGAGGATTCAGCCAGAGCTTACC 579  
595 TGTCCACGCTGAGAGAGAGAGAGCTGCTGATGCTGGAGGATTCAGCCAGAGCTTACC 636  
580 CCACT 639  
637 CAACT 696  
640 ACGAGTATCGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 699  
697 ACGAGTATCGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 756  
700 TCTGAGAGATTTCTCATACAGCTGGAGATGCTGATGCTGATGCTGATGCTGATGCT 759  
757 TCTGAGAGATTTCTCATACAGCTGGAGATGCTGATGCTGATGCTGATGCTGATGCT 816  
760 TGGGAGAGCTTCCAGCTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 819  
817 TGGGAGAGCTTCCAGCTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 876  
820 CAGTCTGATTTATTTCTCTATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 879  
877 CAGTCTGATTTATTTCTCTATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 936  
880 TGTCTCCAGCTGCTTCT 939  
937 TGTCTCCAGCTGCTTCT 996  
940 TGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 999  
997 TGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1056  
1000 TATCCAGAGAGATTTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059  
1057 TCTCTCAGAGAGATTTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1116  
1060 ACGAGCTGTACAGAGATGATTTGATTTCTGAGGAG-----GAGCTAAATCCCTGA 1113  
1117 GATGATGCTGTCT 1176  
1114 ACGAGAGAGAGCTTCT 1173  
1177 ACGAGAGAGCTTCT 1236  
1174 TTAGTCT 1233  
1237 TCATGTCATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1296  
1234 CT 1293  
1297 CT 1356  
1294 CAGCTTATATTAACAGCTGCTGATTTATTTATTTATTTATTTATTTATTTATTTATTT 1353  
1357 CAGCTTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1416  
1354 CAGTCT 1413  
1417 CTGCT 1476  
1414 ACTTCT 1473  
1477 ATTTATTTGCTTACAGTCTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1536  
1474 TGTCTGTATGCTTACTGCTGATCTTACCAACCTCTGCTGAGGAGGAGGAGGAGGAGG 1533  
1537 TGTCTGTATGCTTACTGCTGATCTTACCAACCTCTGCTGAGGAGGAGGAGGAGGAGGAG 1596

QY	1534	TCACATCCACGACCCCTCCAGATGGGACAGACATCATTTGGCCCTCTATTGTTTACCTGGGTG	1593
Db	1597	TCAGCTGCACAGCATTCGCCGCTGGGACGACATCTCTGTCTCTCTACTTGTGTTTACCTTGGTG	1656
QY	1594	CTTACCAACAGATGCTGCTCCCTACATCTGTCATGAGGTAGTCTGACGTCTCCGTATTTGGAATCT	1653
Db	1657	CCATAGACGCGTTCCTGCGCTTACATCTTCATGAGGAAGTATGACATCCCTGTGACACCATCC	1716
QY	1654	TCACCCCTTTTTCCTCCGAGAAAGTTTGGGAATGACTCTTCCAGAAACCTTAAGACGATGC	1713
Db	1717	TCACCTGTTTCTCCACAGAGAGCTTGCGTACCCACTCCAGACACCTTAACACGATGC	1776
QY	1714	AGAAAGTGAATGGTTTCAGATCTGTGGAAAAAACAAGACATCTCATATGAGACAGAGAAAA	1773
Db	1777	TAAAGATCAAAAGGAATGAATAACACAGAAAAACTCCAAAGTCACACAAAGATGTTAAAAAGATG	1836
QY	1774	ATC 1776	
Db	1837	GTC 1839	

```

RESULT 13
US-60-466-412-4827
: Sequence 4827, Application US/60466412
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: IAKUBOVA, Olga
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: CLO01466
: CURRENT APPLICATION NUMBER: US/60/466,412
: CURRENT FILING DATE: 2003-04-30
: NUMBER OF SEQ ID NOS: 429241
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 4827
: LENGTH: 3223
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-466-412-4827

```

Query Match	47.6%;	Score 1016.2;	DB 19;	Length 3223;
Best Local Similarity	75.6%;	Pred. No. 1.6e-232;		
Matches 1272;	Conservative 17;	Mismatches 370;	Indels 24;	Gaps 2

QY GGGTTCATCACCACCTAGTGTGCAATTTTCGAGACGGGACAGTGGAGACATGAGGGAGTAC 159

Db GCGGTCCCMGACCCACGAGCGCGCTGTGTGGGCTCTGAGGGGCGGACATGCGGACTACG 234

QY ACGAGTATATGCGCTTCTCGGGGCGAGTGGGGGCGCTTCACGAGGCTCATATCTTCACGCG 219

Db ACGAGTATGACCGCTTCTCGGGGCGAGTGGGGCGCTTCACGAGGCTCATATCTTCTCTCGC 294

QY TCAGCGCCAGCATCATCCCAATGACTTCAATGATGATGATCACTGTTGTTCTCGGGGCGGA 279

Db TCAGCGCCAGCATCATCCCAATGACTTCAACGGGCTTCACGGGCTTCGAGTTCTGATAGGCA 354

QY CCCCAGGAGCACCGCTGTGTGAGTTCGCGGACCGCGCAACTGTAGACAGCGCTTGGCCACAA 339

Db CCCCAGGAGCACCGCTGTGCGGAGTGCAGGACCGCGCAACTGTAGACAGCGCTTGGCGAAAC 414

QY ACAGTGTCCCGCTGTGGGCTGCGGGAGCGGCGGAGAGTGGCCACAGCTCAGACCGCTTACC 399

Db ACAGTGTCCCACTGGGGGCTGCGGGAGCGGCGGAGAGTGGCCACAGCTCAGCGCGCTTACC 474

QY GGGCTGCGCACCATGTGCGCAATTCTCTGGCGCTCGGGCTGTGAGCGCGGGGCGGAGCTGTGACC 459

Db GGGCTGCGCACCATGTGCGCAATTCTCTGGCGCTCTGTGGCGCTGTGAGCGCGGGGCGGAGCTGTGACC 534

QY TGGGGCAGCTGTGAGGAGGAGGAGAGCTGCTGTGAGTGGCTGTGAGGAGTTCACTCAGAGAGCTTACC 519

Db TGGGGCAGCTGTGAGGAGGAGGAGAGCTGCTGTGAGTGGCTGTGAGGAGTTCACTCAGAGAGCTTACC 594

QY	520	IGTCCACGCGTCACGACGAGGAAATCGGTGGTGTAGGACCACTGGAAAGTCCCTCTCA	579
Db	595	TTGTCACCATTTGTGAACC-----GAGGACGACTGGAAAGGCCCACTCA	636
QY	580	CCACCTCCCTCTCTTTCGTAGGCGTGCCTCGGCTCCCTCGTGTCCGGGACCTGTCA	639
Db	637	CAATCTCCTTCTTCTGTGGTGGTGCCTGTGGGCTCCTTCATTTTCAGGGCACCTGTCA	696
QY	640	ACAGGTTTGGCAGAGAACCTTCTTTCGCAACCATAGGCTGTACAGACTGGCTTCA	699
Db	697	ACAGGTTTGGCGYRGAAGAAATGTGCTGTTCCGACCAATGGCGCTGCACACAGGCTTCAGCT	756
QY	700	TCTCGACAGATTTTCCCATCTGAGCTGGGAGATGTTCACCTGTGTATTTGTATCGTGGGCA	759
Db	757	TCTCTCAGATCTCTCTCGAAGAAATTTTGAAGATGTTTGTGCTGTCTTTGTCTGTGTAGCA	816
QY	760	TGGCGCAGATCTCCAACTATGTGTAGCTTCACTACTAGACAGAAATTTCTTGCGCA	819
Db	817	TGGCGCAATCTCCAACTRTGTGGCAGGATTTTCTCGGGGACAGAAATTTCTTGCGCA	876
QY	820	CAGTTCGATTAATATCTCTCATTTAGAGTGCACATTTTTCAGTTGGCGATATATGC	879
Db	877	CAGTTCGATTAATATCTCTCATTTAGAGTGCATATTTTATATGCAATTTTGTCTACATATGC	936
QY	880	TGCTTGCCACTGTGTTGCTTACTTTCATCAGACACTGGCGGATCTGCTGTGGCGTGA	939
Db	937	TGCTTGCCACTGTGTTTCTTACTTTCATCAGACACTGGCGGATCTGCTGTGGCGTGA	996
QY	940	TGCCGGGAGTCTGTGTCTCCCGCGTGGTGTTCATTTCTGAAATCTCCCGAGGGCTGA	999
Db	997	TGCCGGGAGTCTGTGTCTCCCGCTGCTGTGGTGTTCATTTCTGAAATCTCCCGAGGGCTGA	1056
QY	1000	TATCCCAAGAGAATTTTGTAGAGAGGCTGAAGATATATCATCCAAAAGCTGCAAAATATGACA	1059
Db	1057	TCTCTCAGGAGAGATTTTGAAGGCGAGAGGTATCATCCGCAAGGCTGTMCAAAACCAATG	1116
QY	1060	ACACAGCTGTACACAGCTGATATTTGATTTCTGTGGAG-----GAGTAATATCCCTGA	1113
Db	1117	GGATTTGTGTGCTTCCACTATCTTTGACCCGAGAGTATTCAAAGACTTAAGTTCCAGA	1176
QY	1114	AGCAGCAGAAAGCTTTCATTCGACCTGTTCAGAGCTCGGAAATATTCGCAATATGACA	1173
Db	1177	AGCAGCAGTCCCAACAACTTCGTGAAATCTGTCTTCGAACTGGAAATATCCGAGTGTACACA	1236
QY	1174	TTATGTCTTGTGCTGTATGATGTGTACCTCAGTGGGTTACTTGTCTGTCTGTGATG	1233
Db	1237	TCATGTCCAAATATGCTGTGGATGACCAATATCAGTGGGAAATTTTGGGCTTTCGGTTGATA	1296
QY	1234	CTCCCAATTTACATGAGATGTGCTACGCTGAAGCTGTTTCTCTCGCGCTTGATTAATATC	1293
Db	1297	CTCTCTACTTTCGATGGGACATCTTTTGTGAAGTCTTCTTTCACAGCATGGTTGAAGTCC	1356
QY	1294	CAGCTTAACTTACAGCTTGGCTGTATTGCGAACGCTGCCAGGCGTTATATCATATGCTG	1353
Db	1357	CAGCAATATGTGTCGCTGGCTGTGCTGTGCAATATTTTGCCTCCCGGGCTATTCATCAGTGCCA	1416
QY	1354	CAGTACTGTCTGGGAGAGAGGTGTGCTCTCTTCATTCAACTGGTACTGTGATTAAT	1413
Db	1417	GTGCGCTCTCTCGGTGGGACAGTGTCTCTCTTATGACAGTGTGTACCCCAAGCTGTGT	1476
QY	1414	ACTTCTTATCATTTGGTGTGTGTCATGCTGGGAAATTTTGGATCATCCTGTCTTTCACA	1473
Db	1477	ATTATTTTGGCTACAGTCCGCTGTGTATGTTGGGCAATTTTGGATCATCAGGCTGTCTTTCACA	1538
QY	1474	TGCTGTATGTCTTACACTGTGTAGCTCTACCCAACTCTGTGTAGGAAACATGTGGCGTGGGG	1533
Db	1537	TGCTGTATGTGTACACAGCGCRAAGCTGTATCCACAGTGGTGTAGAAACATGTGGTGTGGAG	1596
QY	1534	TACACATCCAGGCGTCCAGAGTGGGACAGATCATTTGCCCTACTTTTATTTACCTCGGTG	1593
Db	1597	TGACGTSCACAGCATTCGCCCTCGGGGACAGATCTGTCTCTCTCTCTCTTACCTGTGGTG	1656
QY	1594	CTTACCAACGAATGCTGCCCTCATGTCATGTCATGAGTGTCTGTGACTGTCTGTGATTTGGAATCT	1653



Db 1557 CCTAGAGACCGCTTCTGCTTACATTCATGGGAGCTGACCATCTGACAGCCATTC 1716  
QY 1654 TCACCTTTTTCCTGAAAGTTTGGGAATGACTTCCAGAAACCTTGAGAGATGC 1713  
Db 1717 TCACCTGTTTCTCCAGAGAGCTTCGCTACCCACCTCCAGACACCATTCAGAGATGC 1776  
QY 1714 AGAAATGAAATGTTGATCTGGAAGAAAAACAGAGACTCAATGAGAGAGAGAA 1773  
Db 1777 TAAAGTCAAAAGAAATGAAACAGAAAACTCAAGTCAACAGAGATGTAAAGATG 1836  
QY 1774 ATC 1776  
Db 1837 GTC 1839

RESULT 14  
US-10-144-771-9977  
; Sequence 9977, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 9977  
; LENGTH: 2574  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-144-771-9977

Query Match 46.6%; Score 994; DB 14; Length 2574;  
Best Local Similarity 75.7%; Pred. No. 3e-227;  
Matches 1247; Conservative 0; Mismatches 395; Indels 6; Gaps 1;

QY 130 GAGGGAGTGGGAGAGATGCGGGAGTACAGACAGAGTATCGCTTCCGTGGAGATGG 189  
Db 99 GGGAGGCTGAGAGAGCGCATCGGAGACTACAGACAGAGTGAACCGCTTCTAAGGGAATGG 158  
QY 190 GGGCCCTTCAGCGCCTCATCTTCTCTGCTCAGCGCCAGCATCATCCCAATGGCTTCA 249  
Db 159 GGGCCCTTCAGCGCCTCATCTTCTCTGCTCAGCGCCAGCATCATCCCAATGGCTTCA 218  
QY 250 ATGTATGTAGTGTCTGTTCTTGGGGGAGACCCGAGAGACCGGTGTGATGCGCGAG 309  
Db 219 ATGTATGTATCATCTGTTCTTGGGGGAGACCCGAGAGACCGGTGTGATGCGCGAG 278  
QY 310 CCGGAGACCTGAGCAGCGGCTGGGCAACAAGATGTCGGCTGGCGGCTGGCGAGCGCC 369  
Db 279 CCGTGAACCTGAGCAGCGGCTGGGCAACAAGATGTCGGCTGGCGGAGCGAGC 338  
QY 370 GCGAGGTGCCCAAGCTGACAGCGCTACCGGCTCGCCACCATTCGCCAATCTTGGGCGC 429  
Db 339 GACAGGTGCCCTCAAGATGCGGCGCTACCGAGTGGCCACCATTCGCCAATCTTGGGAGC 398  
QY 430 TCGGCGTGGAGCGGGGCGCGAGCTGAGACTTGGGCGAGCTGAGAGCAGAGACTGGCTGG 489  
Db 399 TAGGCGTGGAGCGGGGCGGAGAGTGAAGCTGAGAGAGCTGAGAGCAGAGACTGGCTGG 458  
QY 490 ATGGCTGGAGTTCAACGAGAGAGTGTACTGTGCCACCGTGGAGCGGAGAGAGTGG 549  
Db 459 ATGGCTGGAGTGTCAAGAGAGAGTGTCTTCTGTCCACCATTCGTGAGAGAGTGGAGCTGG 518  
QY 550 TGTGTGAGAGACAATGGAAGGTGGCCCTCACACACTTCCCTGTTCTTCTGAGCGTGGCTCC 609  
Db 519 TGTGTGAGAGATGATGGAAGGCCCTCACACACTTCTTCTTCTGAGCGTGGAGCTGA 578  
QY 610 TGGGCTCTTCTGTTCCGGGAGCTGTCAAGAGGTTTGGCAGAGAAAGCTTCTCTTCG 669  
Db 579 TGGGCTCTTCTGTTCAAGAGAGCTTCTCAAGAGGTTTGGTGGCAAGATATGCTGTTT 638  
QY 670 CAACATGAGCTGTACAGACTGGCTTCAAGTCTTCTGCAAGTATTTCTCCATCAGCTGGAGA 729

Db 639 TGACCATGGGACATGAGACTGGCTTACGTTCTCTGAGAGCTTCTCTGTGAACTTCGAGA 698  
QY 730 TGTTCATCTGTATTTATTCATCTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGG 789  
Db 699 TGTTCATCTGTATTTATTCATCTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGG 758  
QY 790 TCAATAGTAAAGAAATCTTGGCAAGTGGTGTATTTATTCATCTGATCATATGAG 849  
Db 759 TGTCTGGGAAACAGAAATCTTTCAGAGTGGTGTATTTATTCATCTGATCATATGAG 818  
QY 850 TGTGACATTTTGGAGTGGCTATATGCTGTGCTGCACTGTTGCTTACTTATCATCAGAG 909  
Db 819 TTTGATATTTATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 878  
QY 910 ACTGGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969  
Db 879 ACTGGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 938  
QY 970 GGTTCATCTGAAATCTCCCGATGAGCTGATATCCAGAGAAATTTAGAGAGCTGAG 1029  
Db 939 GGTTCATCTGAGTCCAGATCCAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 998  
QY 1030 ATATCATCCAAAAGCTGCAAAATGAACACACAGCTGTACACAGCTGATATTTGAT 1089  
Db 999 TGATCATCCGAAAGCTGCAAAATGAACAGAGTGTGACACTTCCACTATCTTGCATTC 1058  
QY 1090 CTGTGAG-----GAGCTAAATCCCTGGAAGCAGACAGAAAGCTTCTATTCGACTGT 1143  
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QY 1264 ACTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323  
Db 1239 ACTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1298  
QY 1334 GAACGCTGCCAGGCGTATATATCATAGCTGCACTGCTTGGGAGAGAGTGGCTTC 1383  
Db 1299 AGTACTTCCCGGAGATATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1358  
QY 1384 TCTTATTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443  
Db 1359 TCTTATTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1418  
QY 1444 GAAATTTTGGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1503  
Db 1419 GGAAGTTTGGATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1478  
QY 1504 CAACCTGTGAGGAACATGCGGTTGGGGGTACATCCAGCGCTCCAGAGTGGGAGCA 1563  
Db 1479 CCACCTGTGAGGAACATGCGGTTGGGGGTACATCCAGCGCTCCAGAGTGGGAGCA 1538  
QY 1564 TCATTTGCCCCCTACTTGTGTTTACCTGCTGCTTCAACAGAGTCTGCTCCCTACATGCTCA 1623  
Db 1539 TCTGCTGCTCCCTACTTGTGTTTACCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1598  
QY 1624 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1683  
Db 1599 TGGGAAGTCTACCATCTCTGACAGCTATCTCTCACTTGTCTTCTCTGAGAGCTTGTGGT 1658  
QY 1684 TGACTCTTCAGAAACCTTACAGAGATGCAAGAAAGTGAATGCTTCAGATCTGCGAGAA 1743  
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QY 1744 AAACAGAGACTCAATGAGAGAGAGA 1771





Db 1464 CCACTGTGTGACAGAAACATGGGTGTGGGGGTGACGTCCACAGCATCCCGCTTGGAGCA 1523  
QY 1564 TCATGGCCCCCTACTTGTGTACCTGGGTCTTACAACAGAAATGCTGCCCTACATGTCA 1623  
Db 1524 TCCGTCTCCCTACTTGTCTACCTTGTGTGATGATGCTTCCCTTATATCTCA 1583  
QY 1624 TGGTAGTCTGACTGTCTGATTGAAATCTTCACTTTTTCCTGAAAGTTGGAA 1683  
Db 1584 TGGGAAGCTGACCATCTGACAGCTATCTCTACCTTGTCTTCCAGAGAGCTTGTG 1643  
QY 1684 TGACTCTTCCAGAAACCTTAGAGCAGATGCAAGAGTGAATGTTGAGATCTGGGAAA 1743  
Db 1644 CCCCTCTCCCGACACCATGACGATGCTCAGGGTCAAAAGGATATAAACATGGCAAA 1703  
QY 1744 AAACAAGAGCTCATGAGAGACAGAGA 1771  
Db 1704 TCCAAAGCCAAACAGAGAGCAAAAAGA 1731

Search completed: July 5, 2003, 08:54:51  
Job time : 1590 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2003, 12:29:59 ; Search time 18 Seconds  
(without alignments)  
900.668 Million cell updates/sec

Title: US-09-521-195B-1

Perfect score: 2845  
Sequence: 1 MKDDEVIAFLGEMGFQRL.....KTRDSMETENPKVLTAF 551

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCtus.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	702	24.7	555	3	US-08-501-572-3
2	702	24.7	555	3	US-09-040-444-3
3	687.5	24.2	556	3	US-08-501-572-1
4	687.5	24.2	556	3	US-09-040-444-1
5	680	23.9	553	3	US-08-501-572-2
6	680	23.9	553	3	US-09-040-444-2
7	630	22.1	537	2	US-08-647-397-2
8	606.5	21.3	545	4	US-09-572-147-2
9	586	20.6	550	4	US-09-330-245A-2
10	267	9.4	520	4	US-08-964-127-2
11	267	9.4	520	4	US-09-496-692-2
12	234.5	8.2	494	2	US-09-031-392-5
13	234.5	8.2	494	4	US-09-299-549-5
14	234.5	8.2	494	4	US-09-610-417-5
15	222	7.8	492	2	US-08-355-844-3
16	222	7.8	492	2	PCT-US95-16126-3
17	216	7.6	493	2	US-09-031-392-10
18	216	7.6	493	4	US-09-299-549-10
19	216	7.6	493	4	US-09-610-417-10
20	216	7.6	510	4	US-09-291-922-22
21	213.5	7.5	524	2	US-08-928-692-12
22	213.5	7.5	524	4	US-09-339-972-12
23	213.5	7.5	529	4	US-09-291-922-28
24	206.5	7.3	549	4	US-09-291-922-30
25	204.5	7.2	536	4	US-09-291-922-26
26	203	7.1	289	4	US-08-964-127-4
27	203	7.1	286	4	US-09-496-692-4

28	196	6.9	323	4	US-09-134-001C-4635	Sequence 4635, Ap
29	196	6.9	500	2	US-09-031-392-7	Sequence 7, Appl1
30	196	6.9	500	4	US-09-299-549-7	Sequence 7, Appl1
31	196	6.9	500	4	US-09-610-417-7	Sequence 7, Appl1
32	194	6.8	513	4	US-09-291-922-20	Sequence 20, Appl1
33	188.5	6.6	523	4	US-09-291-922-24	Sequence 24, Appl1
34	181	6.4	509	2	US-09-031-392-6	Sequence 6, Appl1
35	181	6.4	509	4	US-09-299-549-6	Sequence 6, Appl1
36	181	6.4	509	4	US-09-610-417-6	Sequence 6, Appl1
37	174.5	6.1	584	2	US-08-928-692-13	Sequence 13, Appl1
38	174.5	6.1	584	2	US-09-339-972-13	Sequence 13, Appl1
39	172	6.0	383	2	US-09-031-392-3	Sequence 3, Appl1
40	172	6.0	383	4	US-09-299-549-3	Sequence 3, Appl1
41	172	6.0	383	4	US-09-610-417-3	Sequence 3, Appl1
42	170.5	6.0	470	4	US-09-134-001C-4610	Sequence 4610, Ap
43	169.5	6.0	488	2	US-08-928-692-11	Sequence 11, Appl1
44	169.5	6.0	488	2	US-09-339-972-11	Sequence 11, Appl1
45	168.5	5.9	488	2	US-08-928-692-10	Sequence 10, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-501-572-3  
; Sequence 3, Application US/08501572  
; Patent No. 6063623  
; GENERAL INFORMATION:  
; APPLICANT: Koepsell, Hermann  
; APPLICANT: Grundeman, Dirk  
; APPLICANT: Gorboulev, Valentin  
; TITLE OF INVENTION: Transport protein which effects the  
; TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals,  
; TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSSEE: Finegan,Henderson,Farabow,Garrett & Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/501,572  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Toohy, Kimberlin M  
; REGISTRATION NUMBER: 35,391  
; REFERENCE/DOCKET NUMBER: 02481.1453-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)408-4000  
; TELEFAX: (202)408-4400  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 555 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-501-572-3

Query Match 24.7%; Score 702; DB 3; Length 555;  
Best Local Similarity 33.7%; Pred. No. 9.9e-65;  
Matches 187; Conservative 93; Mismatches 229; Indels 46; Gaps 14;  
5 DEVIAFLGEMGFQRLIF---LLSAILPENGNGSVVFLACTPERRCPDANTS-- 59  
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Db      6 DVLHGEHFHFOKOMFLLALLSATFAP---IYGVIFLGPDPHRCRSPGVAELSLR 62
QY      60 SAMR-----NNSVPLRLDGRREVHSCRYRLA-TIANFSALGLEPGRVDVGOLEQESC 113
Db      63 CGWSPAELNTYVPGPGPAGASPRQCRREYEDMNOSTPDCVDPLASLDTNRSRLPLGPC 122
QY      114 LDGMEFSQDYLSTVVTENMLVCEDNMKVPLTSLFEVGLSGFVSGQLSDRFGRKNVL 173
Db      123 RDGWY--ETPGSSIVTEFNLVCANSMMLDFQSSVNVGFEFGMSIGYIADRFGRKLC 180
QY      174 FATMAVQTGFSEFLQISWEMFTVLFVYVGMQISNYVAFLGTELLGKSVRIITSTL 233
Db      181 LTTVLINAAAGVLMALSPYTMMLIFRLIOGLVSKAGWLIIGYILITEFVGGRY--RTV 237
QY      234 GVC--TFFAVGYMLPLFAFIRDMRMLLALTVPGLVCPUMWFIPESPRMLISQRRFR 291
Db      238 GIFYVAYTYGVLVAGVAVLPHRMWLOFTVALPFFLLTYWCIIPESPRMLISQKNNA 297
QY      292 EADIIQAKAKMNTAVPAVI-----FDSVEELNPLKQOKAFILDLEFTRNIAIMTMS 345
Db      298 EAMRIIKHAKKNGKSLPASLQRLLEETGKKLNP-----SFLDVRTPOIRKHTMIL 351
QY      346 LLLMMLTSVGFALSADAPNLHGD-AYNCLFSALIEIPAYITAMLLRTLPRTIYAAV 404
Db      352 MYNMTSSVLYOGLIMHM-GLAGDNITYLDFEYSALVEFPAEMILLIIRIGRRYPMAAS 410
QY      405 LFWGGVLLFIQLVVDYFSLISGLVMLGKFGITSASFMLYFAELPVLVNNAAVGYT 464
Db      411 NMVAGAACLASVFIQGLQWLKTIISCLGRMGITMAYEIVCLVNAELYPTRIRNLGVHIC 470
QY      465 STASRVGSIAPFYVLYGAYNRM-----LPIYVGSLLVLIIGIFLFPESLGMPLPET 518
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QY      519 LEOMOKVWFRSGK 533
Db      526 IEAENMORPRKKE 540

RESULT 2
US-09-040-444-3
; Sequence 3, Application US/09040444
; Patent No. 6063766
; GENERAL INFORMATION:
; APPLICANT: Koepsell, Hermann
; APPLICANT: Grundeman, Dirk
; APPLICANT: Gorboulev, Valentin
; TITLE OF INVENTION: Transport Protein Which Effects The
; TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals,
; TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040/444
; FILING DATE: March 18, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: O'Connor, Steven P
; REGISTRATION NUMBER: 41,225
; REFERENCE/DOCKET NUMBER: 2481.1453-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000

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; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-040-444-3

Query Match          24.7%; Score 702; DB 3; Length 555;
Best Local Similarity 33.7%; Pred. No. 9.9e-65;
Matches 187; Conservative 93; Mismatches 229; Indels 46; Gaps 14;

QY      5 DEVIATLGEWGPFORLIEF---LISALIPNGFGMSVFLAGPHEHRCRYPDAANDS-- 59
Db      6 DVLHGEHFHFOKOMFLLALLSATFAP---IYGVIFLGPDPHRCRSPGVAELSLR 62
QY      60 SAMR-----NNSVPLRLDGRREVHSCRYRLA-TIANFSALGLEPGRVDVGOLEQESC 113
Db      63 CGWSPAELNTYVPGPGPAGASPRQCRREYEDMNOSTPDCVDPLASLDTNRSRLPLGPC 122
QY      114 LDGMEFSQDYLSTVVTENMLVCEDNMKVPLTSLFEVGLSGFVSGQLSDRFGRKNVL 173
Db      123 RDGWY--ETPGSSIVTEFNLVCANSMMLDFQSSVNVGFEFGMSIGYIADRFGRKLC 180
QY      174 FATMAVQTGFSEFLQISWEMFTVLFVYVGMQISNYVAFLGTELLGKSVRIITSTL 233
Db      181 LTTVLINAAAGVLMALSPYTMMLIFRLIOGLVSKAGWLIIGYILITEFVGGRY--RTV 237
QY      234 GVC--TFFAVGYMLPLFAFIRDMRMLLALTVPGLVCPUMWFIPESPRMLISQRRFR 291
Db      238 GIFYVAYTYGVLVAGVAVLPHRMWLOFTVALPFFLLTYWCIIPESPRMLISQKNNA 297
QY      292 EADIIQAKAKMNTAVPAVI-----FDSVEELNPLKQOKAFILDLEFTRNIAIMTMS 345
Db      298 EAMRIIKHAKKNGKSLPASLQRLLEETGKKLNP-----SFLDVRTPOIRKHTMIL 351
QY      346 LLLMMLTSVGFALSADAPNLHGD-AYNCLFSALIEIPAYITAMLLRTLPRTIYAAV 404
Db      352 MYNMTSSVLYOGLIMHM-GLAGDNITYLDFEYSALVEFPAEMILLIIRIGRRYPMAAS 410
QY      405 LFWGGVLLFIQLVVDYFSLISGLVMLGKFGITSASFMLYFAELPVLVNNAAVGYT 464
Db      411 NMVAGAACLASVFIQGLQWLKTIISCLGRMGITMAYEIVCLVNAELYPTRIRNLGVHIC 470
QY      465 STASRVGSIAPFYVLYGAYNRM-----LPIYVGSLLVLIIGIFLFPESLGMPLPET 518
Db      471 SSMCDIGGITPFLVY----RLTNIMLEPLMVFGLVAGLALLPETKGAALPET 525
QY      519 LEOMOKVWFRSGK 533
Db      526 IEAENMORPRKKE 540

RESULT 3
US-08-501-572-1
; Sequence 1, Application US/08501572
; Patent No. 6063623
; GENERAL INFORMATION:
; APPLICANT: Koepsell, Hermann
; APPLICANT: Grundeman, Dirk
; APPLICANT: Gorboulev, Valentin
; TITLE OF INVENTION: Transport Protein Which Effects The
; TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals,
; TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

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ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/501,572  
 FILING DATE:  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Toohy, Kimberlin M  
 REGISTRATION NUMBER: 35,391  
 REFERENCE/DOCKET NUMBER: 02481.1453-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)408-4400  
 TELEFAX: (202)408-4400  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 556 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-501-572-1

Query Match 24.2% Score 687.5; DB 3; Length 556;  
 Best Local Similarity 33.2%; Pred. No. 3.3e-63;

Matches 184; Conservative 88; Mismatches 230; Indels 53; Gaps 11;

1 MRDDEVIAFLGEMGPORLIFFLL--SASIIPIGFGMSVFLAGTPHRCRVPDAN 57  
 1 MPTVDVLEQVGEFEMFOKQAFLLCLISASLAP--IYGVIFLGFTPGHYCQNPVAV 57  
 58 LSS--AMR-----NNSVP-LRLRDGRVPHSCSRRL-----ATTANFSAL 95  
 58 LSQRCGMSQAEELNTYVPGIAPSDEASFLSQCKRYEDNMQSLDCVPLSLVANSQ 117  
 96 GLEPRDVLGQLQESCLDGEFSQDYLSTVVTENMLVCEDNMKVPPLTSLFPGVLL 155  
 118 PLGP-----CEHGMY--DTPGSSIVTEFNLCGDAKVDLFGSCVNLGFPL 162  
 156 GSFVSGQLSDRFGRKNVLFATMAVOTGFSFLQISISWEMFTVLFVIYVGGQISNYVAF 215  
 163 GSLVVGYLADRGRIKCLLVTLVTSVSGVLTAVADYTSMLFRLQGMVSKSGMSVSGY 222  
 216 ILGTEIGKSVR-----IIFSTIGVCTFFAVGVMILPLFAVFIKRMRLILATVPGLCY 271  
 223 TLITFEVSGYKRTTALILQMA-----FTVGLVGLAGVAVAIIDRMRLQLAVSLPTFLFL 277  
 272 PLWMTIPESPRWLISQRRFREADIIOKAAKMNNTAVPAVIFDSVEELNPLKQOKAFILD 331  
 278 LYWFVESPSPRWLLSQKRTTRAVRIMEDQAKNGKVPADLKMCLLEDDASEKRSPPAD 337  
 332 LFRTRNIAIMTISLLMLTISVGYFALSADAPNIGHDAYLNCFLSALIEIPAYITAML 391  
 338 LFRTPNLRKHTVILMTFMSCAVLQGLIMHGATGANILYDFEYSSIVPEPAFIIIVT 397  
 392 LRTLPRTTIAVLEFWGGVLLFIQLVPDYYFLISIGVLMGKRGITSAFMLVYFAEL 451  
 398 IDRIRITPIASNLVYTAACILMTFIEHMLVNTIACIGRMKATVILEVCCVNLNEL 457  
 452 YPTLVNNAVGVTSASHVGSIIAIFYVY-LGAVNRMPLTYVMGSLFVLIGIFLTFEPES 510  
 458 YPTFIRNLGMVCSALCDLGIFFPFVFERLMEVWQALPLILFGLVGLTAAGAMTLLPET 517  
 511 LGMTPELLEOKKY 525  
 518 KGVALPETIEAENL 532

RESULT 4  
 US-09-040-444-1

Sequence 1, Application US/09040444  
 Patent No. 6063766  
 GENERAL INFORMATION:  
 APPLICANT: Koepsell, Hermann  
 APPLICANT: Grundeman, Dirk  
 APPLICANT: Gorboulev, Valentin  
 TITLE OF INVENTION: Transport of protein which effects the  
 TITLE OF INVENTION: Transport of cationic xenobiotics and/or Pharmaceuticals,  
 TITLE OF INVENTION: DNA Sequences Encoding it And Their Use.  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/040,444

FILING DATE: March 18, 1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: O'Connor, Steven P

REGISTRATION NUMBER: 41,225

REFERENCE/DOCKET NUMBER: 2481.1453-01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)408-4400

TELEFAX: (202)408-4400

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 556 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-040-444-1

Query Match 24.2% Score 687.5; DB 3; Length 556;  
 Best Local Similarity 33.2%; Pred. No. 3.3e-63;  
 Matches 184; Conservative 88; Mismatches 230; Indels 53; Gaps 11;

1 MRDDEVIAFLGEMGPORLIFFLL--SASIIPIGFGMSVFLAGTPHRCRVPDAN 57  
 1 MPTVDVLEQVGEFEMFOKQAFLLCLISASLAP--IYGVIFLGFTPGHYCQNPVAV 57  
 58 LSS--AMR-----NNSVP-LRLRDGRVPHSCSRRL-----ATTANFSAL 95  
 58 LSQRCGMSQAEELNTYVPGIAPSDEASFLSQCKRYEDNMQSLDCVPLSLVANSQ 117  
 96 GLEPRDVLGQLQESCLDGEFSQDYLSTVVTENMLVCEDNMKVPPLTSLFPGVLL 155  
 118 PLGP-----CEHGMY--DTPGSSIVTEFNLCGDAKVDLFGSCVNLGFPL 162  
 156 GSFVSGQLSDRFGRKNVLFATMAVOTGFSFLQISISWEMFTVLFVIYVGGQISNYVAF 215  
 163 GSLVVGYLADRGRIKCLLVTLVTSVSGVLTAVADYTSMLFRLQGMVSKSGMSVSGY 222  
 216 ILGTEIGKSVR-----IIFSTIGVCTFFAVGVMILPLFAVFIKRMRLILATVPGLCY 271  
 223 TLITFEVSGYKRTTALILQMA-----FTVGLVGLAGVAVAIIDRMRLQLAVSLPTFLFL 277  
 272 PLWMTIPESPRWLISQRRFREADIIOKAAKMNNTAVPAVIFDSVEELNPLKQOKAFILD 331  
 278 LYWFVESPSPRWLLSQKRTTRAVRIMEDQAKNGKVPADLKMCLLEDDASEKRSPPAD 337  
 332 LFRTRNIAIMTISLLMLTISVGYFALSADAPNIGHDAYLNCFLSALIEIPAYITAML 391  
 338 LFRTPNLRKHTVILMTFMSCAVLQGLIMHGATGANILYDFEYSSIVPEPAFIIIVT 397



CURRENT FILING DATE: 2000-05-17  
 CURRENT APPLICATION NUMBER: US/03/312,114  
 PRIOR APPLICATION NUMBER: 60/134,879

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; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 545
; TYPE: PRF
; ORGANISM: MUS MUSCULUS
; US-09-572-147-2

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Query Match      21.3%; Score 606.5; DB 4; Length 545;
Best Local Similarity 29.2%; Pred. No. 9.4e-55;
Matches 161; Conservative 105; Mismatches 249; Indels 37; Gaps 12;

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QY 4 YDEVIATLGEWGPORLIFLLSASIIIPNGFNGSVVFLAGTEPHRCRVPDANLS---59
DB 3 FNDLKQGVGVGRFOLLQVITMVAVPRLMLASHMTLQNFATAPAHCRPPANANLSIDGG 62
QY 60 -SARNNSVPLRLDGEVPHSCRYLATIANFSALGLEPGRDVLGQLEQESCDGWE 118
DB 63 LEAM---LPLD-KQGR-PESCLRF-----PPHNGTEAN-----GTGVTPECLDGVY 104
QY 119 FSDQVYLTSTVTENMLVCEDNMKVPLTTSLEFVGVLGSPVSGQLSDRFGKRVLEATMA 178
DB 105 YDNSTFSTVTENMLVCSHRAPQLAQSLEFMGVLLGAMFGYLADRLGRKRVLLNT- 163
QY 179 VQGFES-FLQIFSIWEMFTVLVYVGMQISNYVVAFLIGTEILGKSVRIIFSTLGVCY 237
DB 164 LQTAVSGTCAAFAPNPTVYCIFRLSGMSLASTAINCMTINMEMPIHTRAYVGTG-LIG 222
QY 238 FFAVGMVLLPLFAFIDRMMLLALTVPGLVPLIMFIPESPRMLISORRREADII 297
DB 223 VYSIGQFLAGIAVAVPHMHLQLAVSPFFVAFIYSWPFIESARWSSSGRLDILRLAL 282
QY 298 QKAKMNNATVPA-----VIFDSVEELNPLKQOKAFILDLFRTNIAITMTISLLML 351
DB 283 QVARIRINGKQEBGAKLSIEVLQTSLOKELTLNKGQASAMMLKCPILRLFLSLMLMRA 342
QY 352 TSVGYFALSDAPRLHGDAYLNCFLSALIEIPAYITAMILLRLPRYITIAAVLEWGGV 411
DB 343 TSFAYVGLVMDLGGFVSMYLIQVIFGAVDLPKAFVCFIYNSMGRHPQQLASLLAGIC 402
QY 412 LLEFQVLPVVDYFISGLVMLGKFGITSAPSMLYVFAELYPVLVNMVAVGVSSTARG 471
DB 403 ILVNGIIPRHHITIRTSVLAVLGCCLASNCIFLTGELYPIMINOTGLMGSTMARVG 462
QY 472 SIAPFVYVLYGAYNRLPYVMGSLVYLIGIFLFPESLGMTLPETLEOMQVKKFRS- 530
DB 463 SIYSPILSMATAEFPISIPLEIFGAVPYAASAVTALLPETLIGPLPTVDLKS----RSR 518
QY 531 GKKTROSMETEE 542
DB 519 GKQKQOOLEQOK 530

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RESULT 9
US-09-330-245A-2
; Sequence 2, Application US/09330245A
; Patent No. 6432631
; GENERAL INFORMATION:
; APPLICANT: GILEAD SCIENCES, INC. et al.
; TITLE OF INVENTION: NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER
; FILE REFERENCE: 240.1Pcnew
; CURRENT APPLICATION NUMBER: US/09/330,245A
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/088,864
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/132,267
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 550
; TYPE: PRF

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; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: this information
; OTHER INFORMATION: is not available.
; US-09-330-245A-2

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Query Match      20.6%; Score 586; DB 4; Length 550;
Best Local Similarity 28.1%; Pred. No. 1.3e-52;
Matches 156; Conservative 104; Mismatches 256; Indels 40; Gaps 9;

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QY 4 YDEVIATLGEWGPORLIFLLSASIIIPNGFNGSVVFLAGTEPHRCRVPDANLSAMR 63
DB 3 FNDLKQGVGVGRFOLLQVITMVAVPRLMLASHMTLQNFATAPAHCRPPADANLS---K 59
QY 64 NNSVPLRL-RDGRVPHSCRYRL-----ATIANFSALGLEPGRDVLGQLEQESCD 113
DB 60 NGLEYVLPRLDQOGPESCLRTSPQWGLPLNGTEAN-----GTGATPFC 105
QY 114 LDGWFSDQVYLTSTVTENMLVCEDNMKVPLTTSLEFVGVLGSPVSGQLSDRFGKRVL 173
DB 106 TDGWTIDNSTFSTVTENMLVCSHRALRLAQSLEYVGVLLGAVVFGYLADRLGRKRVL 165
QY 174 FATMAVQGFES-FLQIFSIWEMFTVLVYVGMQISNYVVAFLIGTEILGKSVRIIFST 232
DB 166 ILNT-LQTAVSGTCAAFAPNPTVYCIFRLSGMALAGISLNCMTLNVEMMPIHTRAYCYGT 224
QY 223 LGVCFEFAVGMVLLPLFAFIDRMMLLALTVPGLVPLIMFIPESPRMLISORRPRE 292
DB 225 L-IGYVYSLGQFLAGIAVAVPHMHLQLAVSAPFAPFIYSWPFIESARWSSSGRLD 283
QY 293 AEDIIQKAKMNNATVPA-----VIFDSVEELNPLKQOKAFILDLFRTNIAITMTISL 346
DB 284 TLRALQVARIRINGKREBGAKLSMEVLRLASLOKELTMKGQASAMMLKCPILRLHFLCLS 343
QY 347 LLMMLTSGYFALSDAPRLHGDAYLNCFLSALIEIPAYITAMILLRLPRYITIAAVLF 406
DB 344 MLMFATISRAYVGLVMDLGGFVSYLLIYVIGAVDLPKAVGLFVINSIGRPPQOMALL 403
QY 407 MCGGVLLFQVLPVVDYFISGLVMLGKFGITSAPSMLYVFAELYPVLVNMVAVGVSST 466
DB 404 LAGICILNGVIRPQOSIVRTSLAVLGCCLASNCIFLTGELYPIMINOTGLMGSTMAR 463
QY 467 ASRVGSIIAPFVYVLYGAYNRLPYVMGSLVYLIGIFLFPESLGMTLPETLEOMQVKK 526
DB 464 MARVGSIVSPVLSMTAEIYPSMPLIFYGAVPYAASAVTALLPETLIGPLPTVDLKS-- 521
QY 527 WFRSGKKTROSMETEE 542
DB 522 --RKGRQTRQOQEHOK 535

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RESULT 10
US-08-964-127-2
; Sequence 2, Application US/08964127
; Patent No. 6277565
; GENERAL INFORMATION:
; APPLICANT: Grandearl, Andrew David John
; TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:

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RESULT 11  
 US-09-496-692-2  
 ; Sequence 2, Application US/09496692  
 ; Patent No. 6313271  
 ;  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Grandearl, Andrew David John  
 ; TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE  
 ; TITLE OF INVENTION: MOLECULES  
 ;  
 ; NUMBER OF SEQUENCES: 17  
 ;  
 ; CORRESPONDENCE ADDRESS:

[illegible]



DB 265 NTRQPIITISIMQLSQSGINAVFYSTGI-----EKDAGVOEPPYATIGA 311  
QY 388 -----AMLLRLTPRRYITAAVLFMG-----GVLLFIQLVPDY-----FLSIG- 428  
DB 312 GVNTIFTVASVFLVERAGRRL--HLIGSGMAFCISLMTISLLKNDYSMSFICIGA 369  
QY 429 -LYMLGKRGITSAFSLVYFAELVPLVRNNAVGTSTAS-----RVGSIAPFYVIG 482  
DB 370 ILVFAAFEEIGPG-PIPMFIVAELEGGPRPAAAVAGCSNMTSNFLVGLLFPSATFYLG 428  
QY 483 AYNRMPLPIYVMSLTVLIGITFLF-FPESIGMTLPE 517  
DB 429 AY-----VFIVTFVPLVFWTFEPKVPETRGTFEE 460

RESULT 14  
US-09-610-417-5  
Sequence 5, Application US/09610417  
Patent No. 6346374  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
Meng, Xun  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING  
GLUTEX AND USES THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: PastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/610,417  
FILING DATE: 05-Jul-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/299,549  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/072002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 494 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-610-417-5

Query Match 8.2% Score 234.5 DB 4 Length 494;  
Best Local Similarity 25.2% Fred. No. 6.7e-16;  
Matches 115; Conservative 76; Mismatches 156; Indels 109; Gaps 23;

QY 133 NLVGEDNMRKVP-----LFTSLFVGVLLGSFVSQGLSDRFGKRN--VFAPTMAY 179  
DB 43 NYTLERSETPSSVLLTSLMSLSVAITSVGMIQSGSVGLFVNFRKNSMLIVNLAI 102  
QY 180 QTG--FSLQIFISISWENFVLVYVGM--GQISNYVAFLIGTEILLKSVRIIFST--- 232  
DB 103 AGGCLMGFCIKI-ABSEVEMLIIGRLIIGFCIGTFVPMYI--GEISPTALRGAFGLINQ 159  
QY 233 LGVCFPAVGVMLLPLFAFYI-----RQMRMLLALIV-PSVLCVPLMWFIPESERWLISO 287

DB 160 LGI-----VIGILVQIDIGLAKVILCTEDLWPLLLGLFTILPILQICAAIPCPESPRLIN 215  
QY 288 RPRE-----AEDIIQKAKANNNAVPAVIDSVBELNPLKQKAFIIDFRTR 336  
DB 216 RKEEKAKKEILLORLMTGEDVNAODIOEMKD-----ESMMSQEKQVLELFRAP 264  
QY 337 N-----IAIMTISLMLMTSGYFALSIDAPNLGDAYINOFALSLEIRAYIT--- 387  
DB 265 NTRQPIITISIMQLSQSGINAVFYSTGI-----EKDAGVOEPPYATIGA 311  
QY 388 -----AMLLRLTPRRYITAAVLFMG-----GVLLFIQLVPDY-----FLSIG- 428  
DB 312 GVNTIFTVASVFLVERAGRRL--HLIGSGMAFCISLMTISLLKNDYSMSFICIGA 369  
QY 429 -LYMLGKRGITSAFSLVYFAELVPLVRNNAVGTSTAS-----RVGSIAPFYVIG 482  
DB 370 ILVFAAFEEIGPG-PIPMFIVAELEGGPRPAAAVAGCSNMTSNFLVGLLFPSATFYLG 428  
QY 483 AYNRMPLPIYVMSLTVLIGITFLF-FPESIGMTLPE 517  
DB 429 AY-----VFIVTFVPLVFWTFEPKVPETRGTFEE 460

RESULT 15  
US-08-355-844-3  
Sequence 3, Application US/08355844  
Patent No. 5940307  
GENERAL INFORMATION:  
APPLICANT: Fischbarg, Jorge  
Applicant: Czegledy, Ferenc  
APPLICANT: Iserovich, Pavel  
APPLICANT: Li, Jun  
APPLICANT: Cheung, Min  
TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN  
STRUCTURE  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/355,844  
FILING DATE: 14-DEC-1994  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Tang, Henry Y.S.  
REGISTRATION NUMBER: 29,705  
REFERENCE/DOCKET NUMBER: A29927-50/29910  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2586  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Human  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..492  
OTHER INFORMATION: Facilitative glucose transporter

OTHER INFORMATION: Glut1 protein  
US-08-355-844-3

Query Match 7.8%; Score 222; DB 2; Length 492;

Best Local Similarity 24.0%; Pred. No. 1.3e-14;  
Matches 117; Conservative 74; Mismatches 175; Indels 122; Gaps 21;

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QY 119 FSDPVLSFYVTENMLVCEENMKPPLTSLFEVGLLGSFVSGQLSDRGRK-----NV 172
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 52 YGESILPTLTLLTMS-----LSVAIFSVGMIGSFVGLFVNRFRGRNSMLMNL 101
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 173 LFAFMVAVQGESFLQFISWEM-----FTVLFEVYVGMGOISNVYVAFLTGT 219
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 102 LAFVSATVLMGFSKL--GKSEMLIGRFLIGVYCGLTGFPVPMYGEVSPTAFRGALGT 158
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 220 ELGKSVRIIEFTLGVCTFPFVAGVMLPLFAVPI---RD-WRMLLALVPGVLCVPLM 274
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 159 -----LHQLGI---VVGILIAQVGLDSIMGNDLWPLLLSIIFIPALLQCIYI 204
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 275 WETPESPRMLISQRRREADITQAKAKNNNTAVPAVIDSVBELNPLKQ-----K 326
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 205 PCPESESPRFLINRNEENRAKSVLK--KLNGTA-----DVTHDLOEMKEESROMREKK 256
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 AFITDLPRTNR-----IAIMTMSLLMMLTSGYFALSIDAPNLHGDAYLNCPLSALI 380
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 VTILELFRSPAYRQPIILIAVYLOLSQOLSGINAVFYSTSI-----FEKAGY 303
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 381 EIPAYIT-----AMLLRLTPRR--YIIAAYLFWGGVLLFTQLVPPVDY-- 423
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 QQPVYATIGGIYNTAFTVYSLFVERAGRRLHLIGLAGMAGQAIIIMTIALALLEQLPW 363
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 424 --FLSIGVLMGKGITSAFS-----MLVFTAEIYPTLVNNAVGVTASRVGS-IIA 475
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 MSTLSIYAI--FGVYAFEEVGPPIPMFTIVAELESQGRPAIIVAGFSNMTSNFTVG 419
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 476 PYEVYLGAVYRMPLIYVMSLTVLIGITFLF--PPESLGMTLPELLEOMQVKWFRSGKKT 534
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 420 MCFQYVQQLCGPYVFIIFVLLVLFIRYFYFKVPETKGRTEDEI-----ASGFRQGGAS 473
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 535 RDSMETEE 542
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 474 QSDKTPPE 481
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Search completed: July 3, 2003, 12:39:03  
Job time : 21 secs